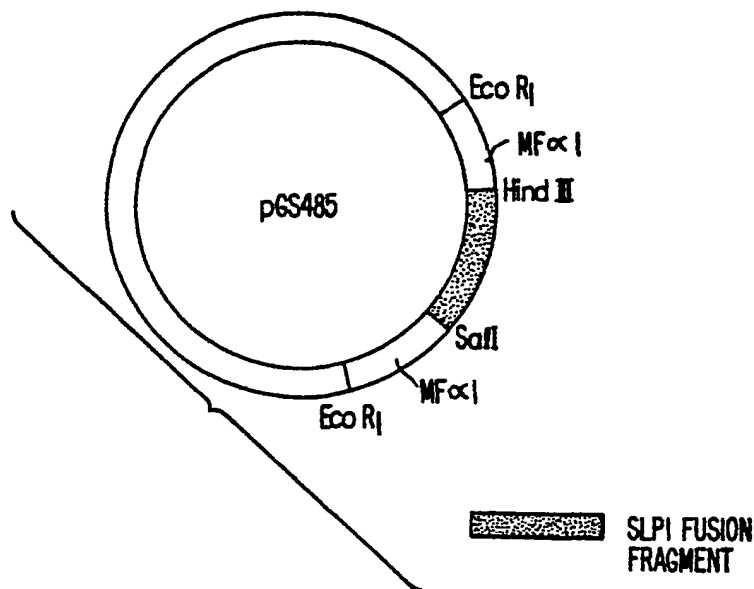




INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁴ : C12P 21/00	A1	(11) International Publication Number: WO 86/ 03519 (43) International Publication Date: 19 June 1986 (19.06.86)
(21) International Application Number: PCT/US85/02385 (22) International Filing Date: 4 December 1985 (04.12.85) (31) Priority Application Numbers: 678,822 803,471 (32) Priority Dates: 6 December 1984 (06.12.84) 2 December 1985 (02.12.85) (33) Priority Country: US (71) Applicant: SYNERGEN BIOLOGICALS, INC. [US/ US]; 1885 - 33rd Street, Boulder, CO 80301 (US). (72) Inventors: BANDYOPADHYAY, Pradip, K. ; 1645 14th Street, Boulder, CO 80302 (US). EISENBERG, Stephen, P. ; STETLER, Gary, L. ; 2325 Panorama Avenue, Boulder, CO 80302 (US). THOMPSON, Robert, C. ; 1120 Drexel Street, Boulder, CO 80303 (US).	(74) Agents: GARRETT, Arthur, S. et al.; Finnegan, Henderson, Farabow, Garrett & Dunner, 1775 K Street, N.W., Washington, DC 20006 (US). (81) Designated States: AT (European patent), AU, BE (European patent), CH (European patent), DE (European patent), DK, FI, FR (European patent), GB (European patent), HU, IT (European patent), JP, KR, LU (European patent), NL (European patent), NO, SE (European patent). Published With international search report.	

(54) Title: RECOMBINANT METHODS FOR PRODUCTION OF SERINE PROTEASE INHIBITORS AND DNA SEQUENCES USEFUL FOR SAME



(57) Abstract

A synthetic DNA sequence and its genetic equivalents which sequences are capable, when used in a recombinant DNA method, of directing production of a serine protease inhibitor protein. Recombinant DNA methods for the production of serine protease inhibitor proteins are also disclosed. These methods incorporate either the synthetic DNA sequence of the present invention or natural DNA sequences isolated from human cDNA or genomic libraries.

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RECOMBINANT METHODS FOR PRODUCTION OF SERINE
PROTEASE INHIBITORS AND DNA SEQUENCES USEFUL FOR SAME

This application is a continuation-in-part of United States Patent Application Serial No. 678,822, filed December 6, 1984.

BACKGROUND OF THE INVENTION

Endogenous proteolytic enzymes serve to degrade invading organisms, antigen-antibody complexes and certain tissue proteins which are no longer necessary or useful to the organism. In a normally functioning organism, proteolytic enzymes are produced in a limited quantity and are regulated in part through the synthesis of protease inhibitors.

A large number of naturally-occurring protease inhibitors serve to control the endogenous proteases by limiting their reactions locally and temporally. In addition, the protease inhibitors may inhibit proteases introduced into the body by infective and parasitic agents. Tissues that are particularly prone to proteolytic attack and infection, e.g., those of the respiratory tract, are rich in protease inhibitors.

Protease inhibitors comprise approximately 10% of the human plasma proteins. At least eight inhibitors have been isolated from this source and characterized in the literature. These include α_2 -macroglobulin (α_2 M), α_1 -protease inhibitor (α_1 PI), α_1 -antichymotrypsin (α_1 Achy), α_1 -anticollagenase (α_1 AC), and inter- α -trypsin inhibitor (I α I).

A disturbance of the protease/protease inhibitor balance can lead to protease mediated tissue destruction, including emphysema, arthritis, glomerulonephritis, periodontitis, muscular dystrophy, tumor invasion and various other pathological conditions. In certain situations, e.g., severe pathological processes such as sepsis or acute leukemia, the amount of free proteolytic enzymes present increases due to the release of enzyme from the secretory cells. In addition, or separately in other situations, a diminished regulating inhibitor capacity of the organism may also cause alterations in the protease/protease inhibitor balance. An example of such a diminished regulating inhibitor capacity is α_1 -protease inhibitor deficiency, which is highly correlated with the development of pulmonary emphysema.

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In organisms where such aberrant conditions are present, serious damage to the organism can occur unless measures can be taken to control the proteolytic enzymes. Therefore, protease inhibitors have been sought which are capable of being administered to an organism to control the proteolytic enzymes.

Leukocyte elastase is an example of a serine protease of particular interest from a pharmacological standpoint. Leukocyte elastase, when released extracellularly, degrades connective tissue and other valuable proteins. While it is necessary for a normally functioning organism to degrade a certain amount of connective tissue and other proteins, the presence of an excessive amount of leukocyte elastase has been associated with various pathological states, such as emphysema and rheumatoid arthritis. To counteract the effects of leukocyte elastase when it is present in amounts greater than normal, a protease inhibitor has been sought which is effective against leukocyte elastase. Such a protease inhibitor would be especially useful if it were capable of being prepared, via a recombinant DNA method, in a purified form and in sufficient quantities to be pharmaceutically useful.

In the past, at least two leukocyte elastase inhibitors have been identified in the literature. One protein, described in Schiessler et al., "Acid-Stable Inhibitors of Granulocyte Neutral Proteases in Human Mucous Secretions: Biochemistry and Possible Biological Function," in Neutral Proteases of Human Polymorphonuclear Leucocytes, Havemann et al. (eds), Urban and Schwarzenberg, Inc. (1978), was isolated from human seminal plasma and sputum and was characterized as being approximately 11 Kda in size with tyrosine as the N-terminal amino acid. The literature reports of this protein have only furnished a partial amino acid sequence, but even this partial sequence indicates that this protein varies substantially from the proteins of the present invention. The reports of the sequence of this protein, in combination with amino acid sequence data for proteins of the present invention, indicate to the present inventors that the product sequenced by Schiessler et al. may have been a degraded protein which was not a single-polypeptide chain.

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A second protein, isolated in one instance from human plasma, has been named α_1 -protease inhibitor. Work on this protein has been summarized in a review by Travis and Salvesen, Annual Review of Biochemistry 52: 655-709 (1983). The reports of the amino acid sequence of this protein indicate that it too differs substantially from the proteins of the present invention.

Because of the substantial differences in structure between single-polypeptide-chain proteins of the present invention and any single-polypeptide-chain serine protease inhibitors of the prior art, the single-polypeptide-chain serine protease inhibitors of the prior art are not "substantially homologous" to the proteins of the present invention.

Trypsin is another protease of particular interest from a pharmacological standpoint. Trypsin is known to initiate degradation of certain soft organ tissue, such as pancreatic tissue, during a variety of acute conditions, such as pancreatitis. Various efforts have been directed toward the treatment of these conditions, without marked success, through the use of proteins which it was hoped would inhibit the action of trypsin. Illustrative of such efforts are attempts to use exogenous bovine trypsin inhibitors in treatment of human pancreatitis. While such techniques have been attempted in Europe, they have not been approved as effective by the U.S. Food and Drug Administration. Thus, there is a need for a protease inhibitor effective in neutralizing excess trypsin in a variety of acute and chronic conditions. As was the case with the leukocyte elastase inhibitor discussed above, a trypsin inhibitor would be particularly useful if it could be isolated and prepared, by recombinant DNA methods, in a purified form and in sufficient quantities to be pharmaceutically useful.

Cathepsin G is another protease present in large quantities in leukocytes. Cathepsin G is known to be capable of degrading in vitro a variety of valuable proteins, including those of the complement pathway. Pancreatic elastase is another protease which may have a role in pancreatitis. Thus, inhibitors for these proteases are also of potential pharmaceutical value.

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Leukocyte elastase, trypsin, cathepsin G and pancreatic elastase are examples of a class of proteases known as serine proteases, which have elements of common structure and mechanism. Their activity against different substrates and their sensitivity to different inhibitors are believed to result from changes in only a few amino acid residues. By analogy, it is possible to conceive of a class of serine protease inhibitors, also having common elements of structure and mechanism, in which changes in a relatively few amino acids will result in inhibition of different proteases, and that at least one member of this class will inhibit every serine protease of the former class. The class of serine protease inhibitors would then be of substantial value.

Surprisingly, the present inventors have discovered a DNA sequence capable of directing synthesis of such a serine protease inhibitor, which inhibitor is biologically equivalent to one isolated from parotid secretions. The protease inhibitor of the present invention, prepared by the recombinant DNA methods set forth herein, is believed to have at least two active sites; one site which exhibits leukocyte elastase inhibiting properties and a second site which exhibits inhibitory activity against trypsin.

The recombinant inhibitor produced by the present invention is believed to be remarkably resistant to denaturation by heat and acids and resistant to proteolytic degradation by a variety of proteolytic enzymes. As used in this application, it is intended that "recombinant inhibitor" refer to a protease inhibitor which is produced by recombinant DNA methodology and techniques. Furthermore, the active form of the recombinant inhibitor of the present invention is thermodynamically stable under conditions that are normally encountered extracellularly in the mammalian body. Denatured forms of the recombinant protease inhibitor also have the ability to form the disulfide bonds and to form the non-covalent interactions necessary to assume an active tertiary structure in the absence of biochemical stimulus.

The DNA sequences of the present invention, set forth more fully hereinbelow, are capable of directing synthesis of a protein which differs greatly from other published leukocyte

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elastase inhibitor sequences. Thus, the identification of the DNA sequence of the present invention has made possible the invention of recombinant DNA methods of manufacturing the novel recombinant protease inhibitors disclosed herein.

Such recombinant methods will allow manufacture of the inhibitors in quantities and purities sufficient to provide economical pharmaceutical compositions which possess serine protease inhibitory activity. Moreover, the identification of the DNA sequence has made possible the invention of recombinant DNA methods of manufacturing analogs of the above described serine protease inhibitor.

SUMMARY OF THE INVENTION

This invention relates to recombinant DNA methods for the manufacture of protease inhibitors generally and, more specifically, to the manufacture of recombinant inhibitors directed to human polymorphonuclear (PMN)-granulocyte proteases. In particular, this invention relates to recombinant DNA methods for the manufacture of inhibitors for human serine proteases, including leukocyte elastase and trypsin.

Additionally, the present invention relates to recombinant DNA methods for the manufacture of analogs of the instant serine protease inhibitors. The present invention also relates to synthetic and natural DNA sequences useful in the recombinant DNA methods as set forth below.

It is an object of the present invention to provide a method for recombinant DNA synthesis of a serine protease inhibitor, which inhibitor is a single polypeptide chain that exhibits serine protease inhibitor activity. These inhibitors possess activity which is biologically equivalent to that activity exhibited by native leukocyte elastase or trypsin inhibitors isolated from human parotid secretions.

To facilitate alternative recombinant DNA syntheses of these serine protease inhibitors, it is a further object of this invention to provide synthetic DNA sequences capable of directing production of these recombinant protease inhibitors, as well as equivalent natural DNA sequences. Such natural DNA sequences may be isolated from a cDNA or genomic library from which the gene

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capable of directing synthesis of the protease inhibitor may be identified and isolated.

Moreover, it is an object of the present invention to provide recombinant DNA methods for the manufacture of analogs of the protease inhibitors discussed above and corresponding analogous DNA sequences useful in such methods.

Additional objects and advantages of the invention will be set forth in part in the description which follows, and in part will be obvious from the description or may be learned from practice of the invention. The objects and advantages may be realized and attained by means of the instrumentalities and combinations particularly pointed out in the appended claims.

To achieve the objects and in accordance with the purposes of the present invention, a DNA sequence has been discovered which is capable of directing the production, by recombinant DNA methodology, of protease inhibitors which, in their active forms, are single-polypeptide-chain proteins that exhibit serine protease inhibitor activity. These recombinant protease inhibitors are remarkably resistant to denaturation by heat and acids. Furthermore, these protease inhibitors retain their biological activity even after exposure to many proteolytic enzymes, such as chymotrypsin, mouse submaxillary protease and clostripain.

The coding strand of a DNA sequence which has been discovered to direct manufacture of these recombinant serine protease inhibitors is:

5'	AGCGG	TAAAA	GCTTC	AAAGC	TGGCG	TATGC	CCGCC
	GAAAA	AATCC	GCGCA	GTGTC	TGCGG	TACAA	AAAAC
	CGGAA	TGCCA	GTCCG	ACTGG	CAGTG	CCCGG	GTAAA
	AAACG	TTGTT	GCCCG	GACAC	CTGCG	GCATC	AAATG
	CCTGG	ATCCG	GTTGA	TACCC	CGAAC	CCGAC	TCGTC
	GAAAA	CCGGG	TAAAT	GCCCG	GTAAC	CTATG	GCCAG
	TGTCT	GATGC	TGAAC	CCGCC	GAACT	TCTGC	GAAAT
	GGACG	GCCAG	TGTAA	ACGAG	ATCTG	AAATG	CTGTA
	TGGGT	ATGTG	CGGCA	AATCT	TGTGT	TTCCC	CGGTA
	AAAGC	ATAA					
							3'

The nucleotides represented by the foregoing abbreviations are set forth in the Detailed Description of the Preferred Embodiment.

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The coding strand for a second, preferred DNA sequence which has been discovered to direct manufacture of these recombinant serine protease inhibitors, particularly a secretory leukocyte protease inhibitor (SLPI) of the present invention, is:

```

5'  TCTGG  TAAAA  GCTTC  AAAGC  TGGCG  TATGC  CCGCC
      GAAAA  AATCC  GCGCA  GTGTC  TGC GG  TACAA  AAAAC
      CGGAA  TGCCA  GTCCG  ACTGG  CAGTG  CCCGG  GTAAA
      AAACG  TTGTT  GCCCG  GACAC  CTGCG  GCATC  AAATG
      CCTGG  ATCCG  GTTGA  TACCC  CGAAC  CCGAC  TCGTC
      GAAAA  CCGGG  TAAAT  GCCCG  GTAAC  CTATG  GCCAG
      TGTCT  GATGC  TGAAC  CCGCC  GAACT  TCTGC  GAAAT
      GGACG  GCCAG  TGTA  ACGAG  ATCTG  AAATG  CTGTA
      TGGGT  ATGTG  CGGCA  AATCT  TGTGT  TTCCC  CGGTA
      AAAGC  ATAA
                                     3'

```

To further achieve the objects and in accordance with the purposes of the present invention, a recombinant DNA method is disclosed which results in microbial manufacture of the instant serine protease inhibitors using either the natural or synthetic DNA sequences referred to above. This recombinant DNA method comprises:

(a) Preparation of a DNA sequence capable of directing a host microorganism to produce a protein having serine protease inhibitor activity, preferably leukocyte elastase inhibitor activity;

(b) Cloning the DNA sequence into a vector capable of being transferred into and replicating in a host microorganism, such vector containing operational elements for the DNA sequence;

(c) Transferring the vector containing the DNA sequence and operational elements into a host microorganism capable of expressing the protease inhibiting protein;

(d) Culturing the microorganism under conditions appropriate for amplification of the vector and expression of the inhibitor;

(e) Harvesting the inhibitor; and

(f) Permitting the inhibitor to assume an active tertiary structure whereby it possesses serine protease inhibitor activity.

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To facilitate identification and isolation of natural DNA sequences for use in the present invention, the present inventors have developed a human parotid tissue cDNA library. This library contains the genetic information capable of directing a cell to synthesize the serine protease inhibitors of the present invention. Other natural DNA sequences which may be used in the recombinant DNA methods set forth herein may be isolated from a human genomic library.

The synthetic DNA sequences useful in the processes of the present invention may be prepared by polynucleotide synthesis and sequencing techniques known to those of ordinary skill in the art. The natural DNA sequences useful in the foregoing process may be identified and isolated through a method comprising:

- (a) Preparation of a human cDNA library from cells, preferably parotid cells, capable of generating a serine protease inhibitor;
- (b) Probing the human DNA library with at least one probe capable of binding to the protease inhibitor gene or its protein product;
- (c) Identification of at least one clone containing the gene coding for the inhibitor by virtue of the ability of the clone to bind at least one probe for the gene or its protein product;
- (d) Isolation of the gene coding for the inhibitor from the clone(s) identified; and
- (e) Linking the gene, or suitable fragments thereof, to operational elements necessary to maintain and express the gene in a host microorganism.

The natural DNA sequences useful in the foregoing process may also be identified and isolated through a method comprising:

- (a) Preparation of a human genomic DNA library, preferably propagated in a recArecBC E. coli host;
- (b) Probing the human genomic DNA library with at least one probe capable of binding to a serine protein inhibitor gene or its protein product;

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(c) Identification of at least one clone containing the gene coding for the inhibitor by virtue of the ability of the clone to bind at least one probe for the gene or its protein product;

(d) Isolation of the gene coding for the inhibitor from the clone or clones identified; and

(e) Linking the gene, or suitable fragments thereof, to operational elements necessary to maintain and express the gene in a host microorganism.

Moreover, to achieve the objects and in accordance with the purposes of the present invention, pharmaceutically useful analogs of the serine protease inhibitor may be produced by the above-recited recombinant DNA method by altering the synthetic DNA sequence or the natural DNA segment, through recombinant DNA techniques, to create a gene capable of inducing expression of the desired analog when cloned into an appropriate vector and transferred into an appropriate host microorganism.

Additionally, to achieve the objects and in accordance with the purposes of the present invention, pharmaceutical compositions containing, as an active ingredient, a recombinant protease inhibitor in accordance with the present invention, or its biologically active analog produced by the above-recited recombinant DNA methods, are disclosed.

The accompanying drawings, which are incorporated herein and constitute a part of this application, illustrate various plasmids useful in this invention and, together with the description, serve to explain the principles of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a map of plasmid pSGE6.

Figure 2 is a map of plasmid pSGE8.

Figure 3 is a map of plasmid pGS285.

Figure 4 is a map of plasmid pGS485.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

Reference will now be made in detail to the presently preferred embodiments of the invention, which, together with the following example, serve to explain the principles of the invention.

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As noted above, the present invention relates to protease inhibitors which have been isolated in a purified form. Preferably, the serine protease inhibitors of the present invention are single-polypeptide-chain proteins which are substantially homologous to, and most preferably biologically equivalent to, native serine protease inhibitors isolated from human parotid secretions. By "biologically equivalent," as used throughout the specification and claims, it is meant that the compositions are capable of preventing protease induced tissue damage of the same type, but not necessarily to the same degree, as the native protease inhibitor. By "substantially homologous," as used throughout the ensuing specification and claims, is meant a degree of homology to the native parotid inhibitor in excess of that displayed by previously reported single-polypeptide-chain serine protease inhibitor proteins. Preferably, the degree of homology is in excess of 40%, most preferably in excess of 50%, with a particularly preferred group of proteins being in excess of 60% homologous with the native parotid inhibitor. The percentage homology as above described is calculated as the percentage of the components found in the smaller of the two sequences that may also be found in the larger of the two sequences, a component being understood as a sequence of four, contiguous amino acids.

Preferred protease inhibitors produced by the present recombinant methods are described in United States Patent Application Serial No. 678,823 of Robert C. Thompson et al. entitled "Serine Protease Inhibitors and Methods for Isolation of Same," filed December 6, 1984 and United States Patent Application Serial No. _____ of Robert C. Thompson et. al. entitled "Serine Protease Inhibitors and Methods for Isolation of Same," filed of even date herewith. Such protease inhibitors are remarkably resistant to denaturation by heat and acids and resistant to loss of activity when exposed to many proteolytic enzymes, including chymotrypsin, mouse submaxillary protease and clostripain. These inhibitors also have the ability to form the necessary disulfide bonds and undergo appropriate non-covalent interactions to assume an active tertiary structure capable of expressing serine

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protease inhibitor activity in the absence of a biochemical stimulus or, if the disulfide bonds have been broken and the non-covalent interactions have been disrupted, to re-form such bonds and interactions to regain such active tertiary structure in the absence of biochemical stimulus.

A preferred serine protease inhibitor having these characteristics has been sequenced. The sequence was determined to be as follows:

Ser-Gly-Lys-Ser-Phe-Lys-Ala-Gly-Val-Cys-Pro-
Pro-Lys-Lys-Ser-Ala-Gln-Cys-Leu-Arg-Tyr-Lys-
Lys-Pro-Glu-Cys-Gln-Ser-Asp-Trp-Gln-Cys-Pro-
Gly-Lys-Lys-Arg-Cys-Cys-Pro-Asp-Thr-Cys-Gly-
Ile-Lys-Cys-Leu-Asp-Pro-Val-Asp-Thr-Pro-Asn-
Pro-Thr-Arg-Arg-Lys-Pro-Gly-Lys-Cys-Pro-Val-
Thr-Tyr-Gly-Gln-Cys-Leu-Met-Leu-Asn-Pro-Pro-
Asn-Phe-Cys-Glu-Met-Asp-Gly-Gln-Cys-Lys-Arg-
Asp-Leu-Lys-Cys-Cys-Met-Gly-Met-Cys-Gly-Lys-
Ser-Cys-Val-Ser-Pro-Val-Lys-Ala.

The foregoing abbreviations correspond to the amino acid residues in the polypeptide as follows:

<u>Amino acid</u>	<u>Abbreviation</u>
Alanine	Ala
Valine	Val
Leucine	Leu
Isoleucine	Ile
Proline	Pro
Phenylalanine	Phe
Tryptophan	Trp
Methionine	Met
Glycine	Gly
Serine	Ser
Threonine	Thr
Cysteine	Cys
Tyrosine	Tyr
Asparagine	Asn
Glutamine	Gln
Aspartic acid	Asp

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Glutamic acid	Glu
Lysine	Lys
Arginine	Arg
Histidine	His

It has been found that these protease inhibitors manufactured by the recombinant DNA methods disclosed herein have more than one distinct domain. By more than one distinct domain it is meant that the protein has multiple active sites which are functional against different enzymes. The presence and location of these sites have been determined by the discovery of a substantial homology between at least two portions of the protease inhibitor. It is believed that the presence of distinct domains confers on the instant protease inhibitors the ability to inhibit a wide variety of serine proteases that includes both leukocyte elastase and trypsin.

It has further been noted that, due to the plurality of distinct domains of these protease inhibitors, the protease inhibitors may serve as frameworks on which various other active sites may be constructed to create protease inhibitors having additional properties. The preferred embodiment of the present invention involves production of a protease inhibitor that inhibits leukocyte elastase, cathepsin G, pancreatic elastase and trypsin. These enzymes are all members of a class of proteases known as serine proteases that share a common mechanism and many structural features. It is believed that, through manipulation of a few amino acid side-chains on the protease inhibitors produced by the present invention, a multiplicity of inhibitors may be created, each being capable of inhibiting at least one member of the whole class of serine proteases. Furthermore, such side-chain modifications can be expected to yield a plurality of inhibitors having improved inhibitory properties with respect to particular members of the class of serine proteases described above.

The amino acid-side chain changes required to attain these goals are suggested by certain elements of structural similarity between the preferred inhibitor produced by the present invention and other serine protease inhibitors for which the

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important functional part of the inhibitor has been elucidated through X-ray crystallography. Those elements of structural similarity include amino acids 17 to 29 and amino acids 70 to 83 of the preferred serine protease inhibitor produced by the present invention described above. The changes suggested to improve the inhibitor's activity, either in terms of quantity or quality, toward trypsin-like serine proteases include changing one or more of amino acid 20 from Arg to Lys, amino acid 72 or 74 from Leu to Lys or Arg, and amino acid 73 from Met to Lys or Arg.

The changes suggested to improve the inhibitor's activity, either in terms of quantity or quality, toward chymotrypsin-like serine proteases, including cathepsin G, include changing one or more of amino acid 20 from Arg to Phe, Tyr or Trp, amino acid 72 or 74 from Leu to Phe, Tyr or Trp, and amino acid 73 from Met to Phe, Tyr, or Trp.

The changes suggested to improve the inhibitor's activity, either in terms of quantity or quality, toward pancreatic-elastase-like serine proteases include changing one or more of amino acid 20 from Arg to Ala, amino acid 72 or 74 from Leu to Ala, and amino acid 73 from Met to Ala.

It must be borne in mind in the practice of the present invention that the alteration of amino acid sequences to confer new protease inhibiting properties on the present proteins may disrupt the inhibitor's activity toward leukocyte elastase or toward trypsin. Such effects may be determined by routine experimentation following the teachings of the present invention.

Further, it is contemplated that substitution of discrete amino acids or of discrete sequences of amino acids, as set forth above, may enhance either the leukocyte elastase inhibitory properties or the trypsin inhibitory properties of the present protease inhibitors while sacrificing some activity of the unenhanced domain. Indeed, the activity of any domain within the inhibitor protein may be eliminated entirely by appropriate amino-acid substitutions, thereby creating inhibitor proteins which are specific for one or some subset of the enzymes against which the protein is normally active. For example, substitution of Gly for Arg in position 20 deactivates the trypsin inhibitory domain

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while substitution of Gly for Met in the 73 position or for Leu in the 72 or 74 position deactivates the leukocyte elastase inhibitory domain. The domains may also be separated into separate proteins, each of which retains the desired inhibitory functions. The present claims extend to other processes for producing such inhibitors by these means.

The present inventors have discovered a synthetic DNA sequence which is capable of directing intracellular production of the above-discussed protease inhibitors. This sequence has the following structure:

```

      HindIII
5'AGC  GGT  AAA  AGC  TTC  AAA  GCT  GGC  GTA  TGC  CCG  CCG
      AluI

      FnuDII      RsaI      HpaII
AAA  AAA  TCC  GCG  CAG  TGT  CTG  CGG  TAC  AAA  AAA  CCG
      HhaI

      XmaI
GAA  TGC  CAG  TCC  GAC  TGG  CAG  TGC  CCG  GGT  AAA  AAA
      HpaII

      NciI
CGT  TGT  TGC  CCG  GAC  ACC  TGC  GGC  ATC  AAA  TGC  CTG
      HpaII      Fnu4HI      BstNI

      BamHI
GAT  CCG  GTT  GAT  ACC  CCG  AAC  CCG  ACT  CGT  CGA  AAA
      HpaII      TagI

      NciI      HpaII      BalI
CCG  GGT  AAA  TGC  CCG  GTA  ACC  TAT  GGC  CAG  TGT  CTG
      HpaII      NciI      HaeIII

ATG  CTG  AAC  CCG  CCG  AAC  TTC  TGC  GAA  ATG  GAC  GGC
      HaeIII

      BglIII
CAG  TGT  AAA  CGA  GAT  CTG  AAA  TGC  TGT  ATG  GGT  ATG
      MboI

      Fnu4HI      NciI
TGC  GGC  AAA  TCT  TGT  GTT  TCC  CCG  GTA  AAA  GCA  TAA 3'
      HpaII

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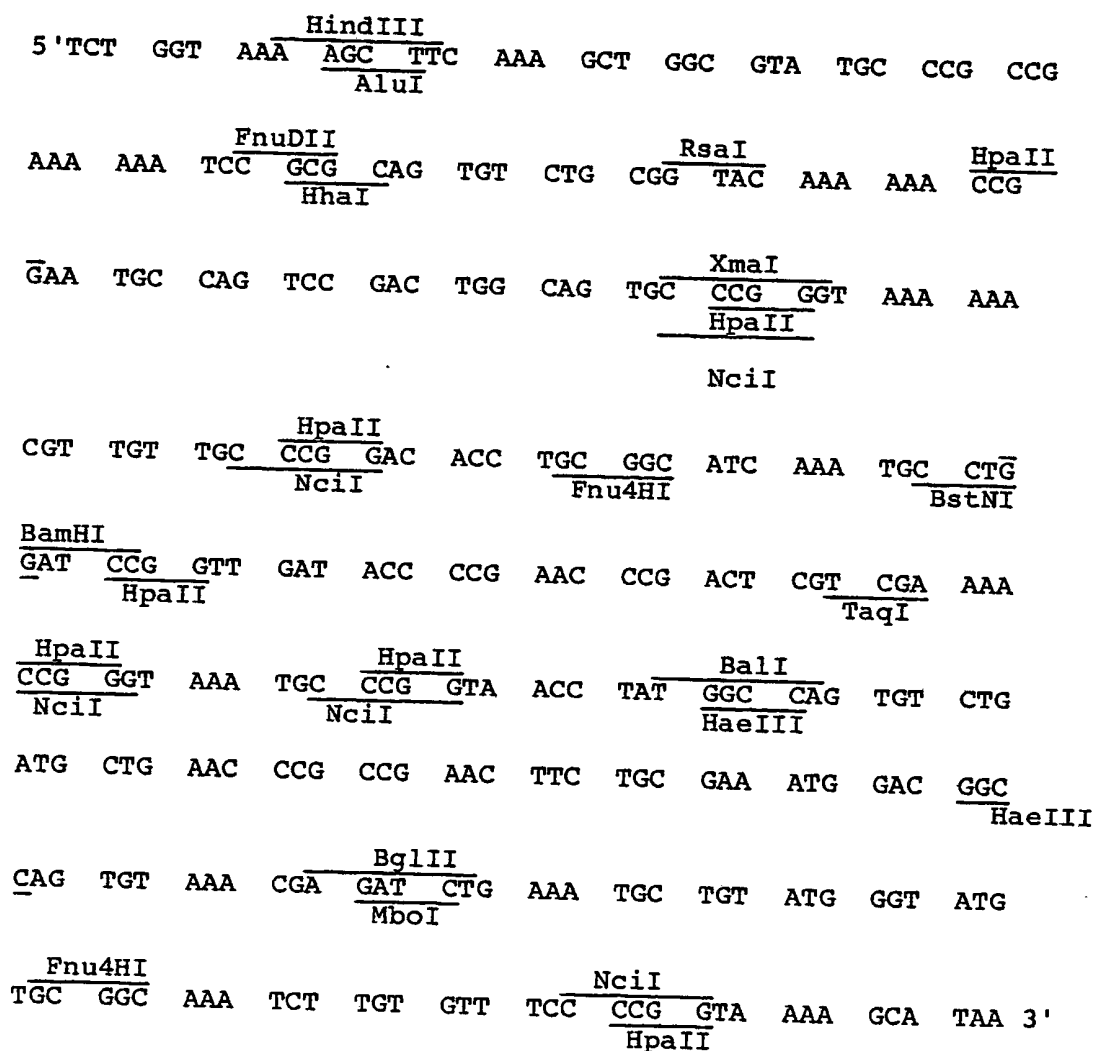
wherein the following nucleotides are represented by the abbreviations indicated below.

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<u>Nucleotide</u>	<u>Abbreviation</u>
deoxyadenylic acid	A
deoxyguanylic acid	G
deoxycytidylic acid	C
thymidylic acid	T

The present inventors have discovered a second, preferred synthetic DNA sequence which is capable of directing extracellular production of the above-discussed protease inhibitors, particularly the secretory leukocyte protease inhibitor (SLPI) referred to above. This sequence has the following structure:



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Due to multiple domain structure of the instant protease inhibitors, as noted above, variations are contemplated in the synthetic DNA sequence set forth herein which will result in a DNA sequence which is capable of directing production of the serine protease inhibitor analogs as discussed above. In particular, preferred analogs of the serine protease inhibitors manufactured by recombinant DNA techniques according to the present invention have the amino acid sequence:

R₁-Gly-Lys-Ser-Phe-Lys-Ala-Gly-Val-Cys-Pro-Pro-Lys-Lys-Ser-Ala-Gln-Cys-Leu-R₂-Tyr-Lys-Lys-Pro-Glu-Cys-Gln-Ser-Asp-Trp-Gln-Cys-Pro-Gly-Lys-Lys-Arg-Cys-Cys-Pro-Asp-Thr-Cys-Gly-Ile-Lys-Cys-Leu-Asp-Pro-Val-Asp-Thr-Pro-Asn-Pro-Thr-Arg-Arg-Lys-Pro-Gly-Lys-Cys-Pro-Val-Thr-Tyr-Gly-Gln-Cys-R₈-R₃-R₉-Asn-Pro-Pro-Asn-Phe-Cys-Glu-R₄-Asp-Gly-Gln-Cys-Lys-Arg-Asp-Leu-Lys-Cys-Cys-R₅-Gly-R₆-Cys-Gly-Lys-Ser-Cys-Val-Ser-Pro-Val-Lys-R₇,

wherein,

R₁ and R₇ are the same or different and are selected from the group consisting of a substituted or unsubstituted amino acid residue or derivative thereof; and

R₂, R₃, R₄, R₅, R₆, R₈ and R₉ are the same or different and are selected from the group consisting of methionine, valine, alanine, phenylalanine, tyrosine, tryptophan, lysine, glycine and arginine.

It should be noted that the DNA sequence set forth above represents a preferred embodiment of the present invention. Due to the degeneracy of the genetic code, it is to be understood that numerous choices of nucleotides may be made which will lead to a DNA sequence capable of directing production of the instant protease inhibitors or their analogs. As such, DNA sequences which are functionally equivalent to the sequence set forth above or which are functionally equivalent to sequences which would direct production of analogs of the protease inhibitor produced pursuant to the amino acid sequence set forth above, are intended to be encompassed within the present invention. As an example of

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the codon substitutions that are contemplated as a result of the degenerate genetic code, the following diagram represents additional DNA sequences which are intended to be included within the scope of the present invention for manufacture of the preferred amino acid sequence enumerated above. By following the example for determining equivalent DNA sequences for production of this protein, those of ordinary skill in the art will be able to determine equivalent DNA sequences for production of analogs of the preferred amino acid sequence as well.

															10																		
Ser	Gly	Lys	Ser	Phe	Lys	Ala	Gly	Val	Cys	Pro	Pro	Lys	Lys	Ser	Ala																		
5'TCN	GGN	AAP	TCN	TTQ	AAP	GCN	GGN	GTN	TGQ	CCN	CCN	AAP	AAP	TCN	GCN																		
AGQ			AGQ												AGQ																		
															20																	30	
Gln	Cys	Leu	Arg	Tyr	Lys	Lys	Pro	Glu	Cys	Gln	Ser	Asp	Trp	Gln	Cys																		
CAP	TGQ	CTN	CGN	TAQ	AAP	AAP	CCN	GAP	TGQ	CAP	TCN	GAQ	TGG	CAP	TGQ																		
		TTP	AGP									AGQ																					
															40																		
Pro	Gly	Lys	Lys	Arg	Cys	Cys	Pro	Asp	Thr	Cys	Gly	Ile	Lys	Cys	Leu																		
CCN	GGN	AAP	AAP	CGN	TGQ	TGQ	CCN	GAQ	ACN	TGQ	GGN	ATQ	AAP	TGQ	CTN																		
				AGP								ATA			TTP																		
															50																	60	
Asp	Pro	Val	Asp	Thr	Pro	Asn	Pro	Thr	Arg	Arg	Lys	Pro	Gly	Lys	Cys																		
GAQ	CCN	GTN	GAQ	ACN	CCN	AAQ	CCN	ACN	CGN	CGN	AAP	CCN	GGN	AAP	TGQ																		
									AGP	AGP																							
															70																	80	
Pro	Val	Thr	Tyr	Gly	Gln	Cys	Leu	Met	Leu	Asn	Pro	Pro	Asn	Phe	Cys																		
CCN	GTN	ACN	TAQ	GGN	CAP	TGQ	CTN	ATG	CTN	AAQ	CCN	CCN	AAQ	TTQ	TGQ																		
							TTP		TTP																								
															90																		
Glu	Met	Asp	Gly	Gln	Cys	Lys	Arg	Asp	Leu	Lys	Cys	Cys	Met	Gly	Met																		
GAP	ATG	GAQ	GGN	CAP	TGQ	AAP	CGN	GAQ	CTN	AAP	TGQ	TGQ	ATG	GGN	ATG																		
							AGP		TTP																								
															100																		
Cys	Gly	Lys	Ser	Cys	Val	Ser	Pro	Val	Lys	Ala																							
TGQ	GGN	AAP	TCN	TGQ	GTN	TCN	CCN	GTN	AAP	GCN	3'																						
			AGQ			AGQ																											

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In the above sequence, abbreviations used are intended to represent the nucleotides indicated below.

<u>Nucleotide</u>	<u>Abbreviation</u>
A,G,C,T	N
A,G	P
C,T	Q

When selecting codons for use in the synthetic DNA sequences of the present invention, including that set forth immediately above, it is preferred that the codons used to indicate a particular amino acid be those which are associated with highly expressed proteins. Examples of these preferred codons are set forth in part in Grantham, R. et al., "Codon Catalog Usage Is a Genome Strategy Modulated For Gene Expressivity" in Nucleic Acids Research 9:r43 (1981). The preferred DNA sequence of the present invention was chosen by selecting Escherichia coli sequence codons for any of the degenerate sequences.

Additionally, it is desired to select codons which facilitate the alteration of the synthetic DNA sequence to construct additional synthetic DNA sequences which are capable of directing production of analogs of the present protease inhibitors. In particular, it is preferred that nucleotide sequences are selected which, if possible, create restriction endonuclease sites at, or close to, positions in the synthetic DNA sequence into which it may be desired to insert additional codons or at which sites it may be desired to replace a codon so that analogs may be created. In the preferred embodiment of the DNA sequence of the present invention, the restriction sites are indicated below the nucleotide sequence set forth above.

Methods of creating the synthetic DNA sequences contemplated herein are generally within the ambit of routine tasks performed by one of ordinary skill in the art guided by instant disclosure. An example of a suitable method which may be used to obtain the synthetic DNA sequence disclosed herein is set forth in Matteacci, M.D. and Caruthers, M.H., J.Am.Chem.Soc. 103:3185 (1981) and Beaucage, S.L. and Caruthers, M.H., Tetrahedron Lett. 22:1859 (1981), both of which are specifically incorporated herein by reference.

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In an alternate embodiment of the present invention, a DNA sequence has been isolated from a human genomic library which encodes a preferred secretory leukocyte protease inhibitor (SLPI) of the present invention. This sequence, encoding from the fourth codon and including the introns as presently known to the inventors, is as follows:

```
EcoRI      .      20      .      40      .      60
GAATTCTGGTGGGGCCACACCCACTGGTGAAAGAATAAATAGTGAGGTTTGGATTGGCC
-----INTRON-----

      .      80      .      100      .      120
ATCAGAGTCACTCCTGCCTTCACCATGAAGTCCAGCGGCCTCTTCCCCTTCCTGGTGCTG
-----

      .      140      .      160      .      180
CTTGCCCTGGAACCTCTGGCACCTTGGGCTTGGAAGGCTCTGAAATGTAAGTTGGAGTCACT
-----

      .      PstI      .      220      .      240
CTGTCTAATCTGGGCTGCAGGGTCAGAGGTGGGGTCTCCTTGTGGTGTGGGTGTGTCCCC
-----

      .      260      .      280      .      300
TTCTGTAGGCTCTGATCCCTCAGCTTAGTTTCGGGAGACCTCCCTGAGGGTGGAATACAT
-----

      SacI      320      .      340      .      360
GTCTGGCTGAGCTCCAAGGTTTGTGTGACAGTTTGAGCTTCTGGAAATGCTTCCTCTATG
-----

      .      380      .      400      .      420
CAGCCATGCTGTCAGCCAGGTCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA
-----

      .      440      .      460      .      480
TACTCCGCCTTCTTCTTCACCTTGCTGCGACTCTCAAATCATTAGTTTCTGACTCTGCTT
-----

      .      500      .      520      .      540
CCGTTGTGTCTTTGCTTCTGCTATTTTGTCTCTGTGCTTCTCGCTTGGGATTTAGCTCTC
-----

      .      560      .      580      .      600
AACTTCTCTCACACTGGTCTATTTATCTTTGTTTACCTCTCTCCATCTCCATCACTCCC
-----

      .      620      .      640      .      660
AGCCTTCCTCTCTGCCTTTGTGTAGCCTTGTTTTGCTCTTGGGTGGAGGTCTTGACTAGA
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      680              700              720
AGCCTGCTGCCCTTTTCTTGGGTGTGAAACGTCCCCTGTCCATTTGTCTAATTTAATCAA
-----

      740              760              780
GCCCATCAATACACCTGGAGATCAGGCAGGCATGACCTTTGGGCTTTGTGGACAGCTACT
-----

      800              820              840
GAGGTAAGGGTCTCTCCCCCTCAAAAGTGGTGCTTTGTTTCAGGAGGCATGATGGGTCCTC
-----

      860              880              900
AGTACCCAGCCTCCTCCTACCTCTTGACTTTCTCTTCAAAGCCTTCAAAGCTGGAGTCT
-----END OF INTRON-----      F K A G V

      920              940              960
GTCCTCCTAAGAAATCTGCCCAGTGCCTTAGATACAAGAAACCTGAGTGCCAGAGTGACT
C P P K K S A Q C L R Y K K P E C Q S D

      980              1000              BamH1
GGCAGTGTCCAGGGAAGAAGAGATGTTGTCCTGACACTTGTGGCATCAAATGCCTGGATC
W Q C P G K K R C C P D T C G I K C L D

      1040              1060              1080
CTGTTGACACCCCAAACCAAGTAAGCAGGTGCGGGAACTGGGTAGAGAGATAGCCTGGG
P V D T P N P -----START INTRON-----

      1100              1120 StuI              1140
GACACAGCATTAGAGGGACGGAACCTGGGTGATGGGTCTGCCAGGCCTCCTTGTCAATGC
-----

      1160              PvuII              1200
CGTAGTGAGTCACAGTGCCCTAAGAGAAGTAGCCAGCTGGTGAAGCAGCGGGCATTAGA
-----

      1220              1240              1260
TAGCCAGGTAGTTGGAAGCCTCCACCTAGTCAGCACTGGGCGGCTGGCACCTGCATAAT
-----

      1280              1300              1320
GGGGGGCCTGAAGTTC TAGGAGAGCCAGGTGCTATGTTTGGGGGCCGCTTAGGGAGAAG
-----

      1340              1360              1380
GTGGTGGTGATAGAGGTGGGGAGGGGATGATCCCCCTGCTGAAGCTGGACGAGGGGCTC
-----

      1400              1420 StuI              1440
ACTCTAAAAAGTGGGGATGGGAGGGGTTGTATAAAGTACAAGGCCTCTGACCGGTAGCCT
-----END OF INTRON-----

      1460              1480              1500
CACTCTCACCCAACCCAGCAAGGAGGAAGCCTGGGAAGTGCCCAGTGACTTATGGCCAAT
-----R R K P G K C P V T Y G Q

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      .      1520      .      1540      .      1560
GTTTGATGCTTAACCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAAGCGTGACTTGA
C  L  M  L  N  P  P  N  F  C  E  M  D  G  Q  C  K  R  D  L

      .      1580      .      1600      .      1620
AGTGTTGCATGGGCATGTGTGGGAAATCCTGCGTTTCCCCTGTGAAAGGTAAGCAGGGGA
K  C  C  M  G  M  C  G  K  S  C  V  S  P  V  K  --START INTRON

      .  SacI 1640      .      1660      .      1680
CGAGGGCACACTGAGCTCCCTCAGCCCTCTCAGCCTCAACCCTCTGGAGGCCCAGGCATA
-----

      .      1700      .      1720      .      1740
TGGGCAGGGGGACTCCTGAACCCTACTCCAAGCACAGCCTCTGTCTGACTCCCTTGTCTT
-----

      .      1760      .      1780      .      1800
TCAAGAGAACTGTTCTCCAGGTCTCAGGGCCAGGATTTCCATAGGAGTCGCCTGTGGCTT
-----

      .      1820      .      1840      .      1860
TGATTCTATTCTAGTGTCTCTGGGTGGGGGTCCTGGGCAAGTGTCTTTCTGAGTCTAGTT
-----

      .      1880      .      1900      .      1920
TCTTTATCGGTAAAATGTACATAATGAGATGAAAGTGCTCTGCAAAGACCTATGTGCACT
-----

      .      1940      .      1960      .      1980
AAGAATTATTATTCAGGTGTTTCCATCATGTTTCTGAGGTGAAATCACAAAGGATCAGT
-----

      .      2000      .      2020      .      2040
GGAGTTTGAGGATTATCTAGTTCAATGCTTTGAGTTTAGAGTTTTACGTGAAAATGAGAC
-----

      .      2060      .      2080      .      2100
TTGTCTCCTGACACTAAGTCTCTCTCAACTATAGCGCTATCTTGCTATTTTCTCTATCTC
-----

      .      2120      .      2140      .      2160
AGAAGGATCCTTGGGCAGGAGGAAGGATGTGGATATATGATTTGGCTGGTCTTCTATGCTG
-----

      .      2180      .      2200      .      2220
AAGCTCTGATCTGATTTTCTCTCACAGCTTGATTCCCTGCCATATCGGAGGAGGCTCTGGA
-PROBABLE----- STOP
      END OF INTRON

      .      2240      .      2260
GCCTGCTCTGTGTGGTCCAGGTCCTTTCCACCCTGAGCTTGGCTCCACCACTGGT

```

In this sequence, the abbreviations used for the amino acid residues are the one-letter abbreviations which are commonly employed

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and may be found, for example, in Biochemistry by A.L. Lehninger, 2nd ed., Worth Publishers, Inc., New York, New York (1976), pg. 72.

Using this sequence and the amino acid sequence data contained herein, a synthetic DNA sequence can be constructed, that, when added to the genomic sequence above, leads to a gene which codes for the entire protease inhibitor. Alternatively, probes may be constructed using the DNA sequence set forth above and used to retrieve a DNA segment from a human genomic library which has codons for the first three amino acids.

Additionally, such probes may be used to identify a human genomic sequence which contains an appropriate leader sequence. It is contemplated that this leader sequence, or any other appropriate leader sequence, could be used in conjunction with this genomic DNA sequence in a mammalian expression system.

In another alternate embodiment of the present invention, a cDNA clone has been isolated from a parotid library which encodes a DNA sequence capable of directing intracellular production of a preferred secretory leukocyte protease inhibitor of the present invention. This clone is included on _____ on deposit at American Type Culture Collection, Rockville, Maryland, under Accession No. _____.

A recombinant DNA method for the manufacture of a protease inhibitor composed of a single polypeptide chain with at least one active site possessing serine protease inhibitor activity has been disclosed. In one embodiment of the invention, the active site functions in a manner biologically equivalent to that of the native leukocyte elastase inhibitor isolated from human parotid secretions. A natural or synthetic DNA sequence may be used to direct production of the protease inhibitors. This method comprises:

(a) Preparation of a DNA sequence capable of directing a host microorganism to produce a protein having serine protease inhibitor activity;

(b) Cloning the DNA sequence into a vector capable of being transferred into and replicated in a host microorganism, such vector containing operational elements for the DNA sequence;

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(c) Transferring the vector containing the synthetic DNA sequence and operational elements into a host microorganism capable of expressing the protease inhibitor;

(d) Culturing the microorganism under conditions appropriate for amplification of the vector and expression of the inhibitor;

(e) Harvesting the inhibitor; and

(f) Permitting the inhibitor to assume an active tertiary structure whereby it possesses serine protease inhibitory activity.

Synthetic DNA sequences contemplated for use in this method have been discussed in detail above. It is further contemplated, in an alternative embodiment, that natural DNA sequences may also be used in this method. These sequences include cDNA or genomic DNA segments. In a preferred version of this embodiment, it is contemplated that the natural DNA sequence will be obtained by a method comprising:

(a) Preparation of a human cDNA library from cells, preferably parotid cells, capable of generating a serine protease inhibitor;

(b) Probing the human DNA library with at least one probe capable of binding to the protease inhibitor gene or its protein product;

(c) Identification of at least one clone containing the gene coding for the inhibitor by virtue of the ability of the clone to bind at least one probe for the gene or its protein product;

(d) Isolation of the gene coding for the inhibitor from the clone or clones chosen;

(e) Linking the gene, or suitable fragments thereof, to operational elements necessary to maintain and express the gene in host microorganism.

The natural DNA sequences useful in the foregoing process may also be identified and isolated through a method comprising:

(a) Preparation of a human genomic DNA library, preferably propagated in a recArecBC E. coli host;

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(b) Probing the human genomic DNA library with at least one probe capable of binding to a serine protein inhibitor gene or its protein product;

(c) Identification of at least one clone containing the gene coding for the inhibitor by virtue of the ability of the clone to bind at least one probe for the gene or its protein product;

(d) Isolation of the gene coding for the inhibitor from the clone(s) identified; and

(e) Linking the gene, or suitable fragments thereof, to operational elements necessary to maintain and express the gene in a host microorganism.

In isolating a natural DNA sequence suitable for use in the above-method, it is preferred to identify the two restriction sites located within and closest to the end portions of the appropriate gene or sections of the gene. The DNA segment containing the appropriate gene is then removed from the remainder of the genomic material using appropriate restriction endonucleases. After excision, the 3' and 5' ends of the DNA sequence are reconstructed to provide appropriate DNA sequences capable of coding for the N- and C- termini of the serine protease inhibitor protein and capable of fusing the DNA sequence to its operational elements.

The vectors contemplated for use in the present invention include any vectors into which a DNA sequence as discussed above can be inserted, along with any preferred or required operational elements, and which vector can then be subsequently transferred into a host microorganism and replicated in such microorganism. Preferred vectors are those whose restriction sites have been well documented and which contain the operational elements preferred or required for transcription of the DNA sequence.

The "operational elements," as discussed herein, include at least one promoter, at least one operator, at least one leader sequence, at least one Shine-Dalgarno sequence, at least one terminator codon, and any other DNA sequences necessary or preferred for appropriate transcription and subsequent

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translation of the vector DNA. In particular, it is contemplated that such vectors will contain at least one origin of replication recognized by the host microorganism along with at least one selectable marker and at least one promoter sequence capable of initiating transcription of the synthetic DNA sequence. It is additionally preferred that the vector, in one embodiment, contains certain DNA sequences capable of functioning as regulators, and other DNA sequences capable of coding for regulator protein. These regulators, in one embodiment, serve to prevent expression of the synthetic DNA sequence in the presence of certain environmental conditions and, in the presence of other environmental conditions, allow transcription and subsequent expression of the protein coded for by the synthetic DNA sequence. In particular, it is preferred that regulatory segments be inserted into the vector such that expression of the synthetic DNA will not occur in the absence of, for example, isopropylthio- β -D-galactoside. In this situation, the transformed microorganisms containing the synthetic DNA may be grown to a desired density prior to initiation of the expression of the protease inhibitor. In this embodiment, expression of the desired protease inhibitor is induced by addition of a substance to the microbial environment capable of causing expression of the DNA sequence after the desired density has been achieved.

Additionally, it is preferred that an appropriate secretory leader sequence be present, either in the vector or at the 5' end of the synthetic DNA sequence. The leader sequence is in a position which allows the leader sequence to be immediately adjacent to the initial portion of the nucleotide sequence capable of directing expression of the protease inhibitor without any intervening translation termination signals. The presence of the leader sequence is desired in part for one or more of the following reasons: 1) the presence of the leader sequence may facilitate host processing of the initial product to the mature recombinant protease inhibitor; 2) the presence of the leader sequence may facilitate purification of the recombinant protease inhibitors, through directing the protease inhibitor out of the cell cytoplasm; 3) the presence of the leader sequence may affect the

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ability of the recombinant protease inhibitor to fold to its active structure through directing the protease inhibitor out of the cell cytoplasm.

In particular, the leader sequence may direct cleavage of the initial translation product by a leader peptidase to remove the leader sequence and leave a polypeptide with the preferred amino acid sequence which has the potential of serine protease inhibitory activity. In some species of host microorganisms, the presence of the appropriate leader sequence will allow transport of the completed protein into the periplasmic space, as in the case of E. coli. In the case of certain yeasts and strains of Bacilli and Pseudomonas, the appropriate leader sequence will allow transport of the protein through the cell membrane and into the extracellular medium. In this situation, the protein may be purified from extracellular protein.

Thirdly, in the case of some of the protease inhibitors prepared by the present invention, the presence of the leader sequence may be necessary to locate the completed protein in an environment where it may fold to assume its active structure, which structure possesses the appropriate elastase-inhibitor activity.

Additional operational elements include, but are not limited to, ribosome binding sites and other DNA sequences necessary for microbial expression of foreign proteins. In a preferred embodiment of the present invention, the sequence GAGGCGCAAAAA(ATG) would be used as the ribosome binding site. The operational elements as discussed herein are routinely selected by those of ordinary skill in the art in light of prior literature and the teachings contained herein. General examples of these operational elements are set forth in B. Lewin, Genes, Wiley & Sons, New York (1983), which is specifically incorporated herein by reference. The vectors as contemplated herein may be constructed in part from portions of plasmids pBR322 and/or pIQ.

In one preferred embodiment of the present invention, an additional DNA sequence is located immediately preceding the synthetic DNA sequence which codes for the protease inhibitor. The additional DNA sequence is capable of functioning as a

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translational coupler, i.e., it is a DNA sequence that encodes an RNA which serves to position ribosomes immediately adjacent to the ribosome binding site of the protease inhibitor RNA with which it is contiguous. In one embodiment of the present invention, the translational coupler may be derived using the DNA sequence TAACGAGGCGCAAAAAATGAAAAAGACAGCTATCGCGATCGGAGTGTAAGAAATG and methods currently known to those of ordinary skill in the art related to translational couplers. A second, preferred translational coupler has the DNA sequence TAACGAGGCGCAAAAAATGAAAAAGACAGCTATCGCGATCAAGGAGAAATAAATG.

Upon synthesis and isolation of all necessary and desired component parts of the above-discussed vector, the vector is assembled by methods generally known to those of ordinary skill in the art. Assembly of such vectors is believed to be within the duties and tasks performed by those with ordinary skill in the art and, as such, is capable of being performed without undue experimentation. For example, similar DNA sequences have been ligated into appropriate cloning vectors, as set forth in Schoner *et al.*, Proceedings of the National Academy of Sciences U.S.A., 81:5403-5407 (1984), which is specifically incorporated herein by reference.

In construction of the cloning vector of the present invention it should additionally be noted that multiple copies of the synthetic DNA sequence and its attendant operational elements may be inserted into each vector. In such an embodiment the host organism would produce greater amounts per vector of the desired protease inhibitor. The number of multiple copies of the DNA sequence which may be inserted into the vector is limited only by the ability of the resultant vector, due to its size, to be transferred into and replicated and transcribed in an appropriate host microorganism.

Additionally, it is preferred that the vector contain a selectable marker, such as a drug resistance marker or other marker which causes expression of a selectable trait by the host microorganism. In a particularly preferred embodiment of the present invention, the gene for tetracycline resistance is preferably included on the cloning vector.

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Such a drug resistance or other selectable marker is intended in part to facilitate in the selection of transformants. Additionally, the presence of such a selectable marker on the cloning vector may be of use in keeping contaminating microorganisms from multiplying in the culture medium. In this embodiment, such a pure culture of the transformed host microorganisms would be obtained by culturing the microorganisms under conditions which require the induced phenotype for survival.

The vector thus obtained is then transferred into the appropriate host microorganism. It is believed that any microorganism having the ability to take up exogenous DNA and express those genes and attendant operational elements may be chosen. It is preferred that the host microorganism be a facultative anaerobe or an aerobe. Particular hosts which may be preferable for use in this method include yeasts and bacteria. Specific yeasts include those of the genus Saccharomyces, and especially Saccharomyces cerevisiae. Specific bacteria include those of the genera Bacillus, Escherichia, and Pseudomonas, especially Bacillus subtilis and Escherichia coli.

After a host organism has been chosen, the vector is transferred into the host organism using methods generally known by those of ordinary skill in the art. Examples of such methods may be found in Advanced Bacterial Genetics by R. W. Davis et al., Cold Spring Harbor Press, Cold Spring Harbor, New York, (1980), which is specifically incorporated herein by reference. It is preferred, in one embodiment, that the transformation occur at low temperatures, as temperature regulation is contemplated as a means of regulating gene expression through the use of operational elements as set forth above. In another embodiment, if osmolar regulators have been inserted into the vector, regulation of the salt concentrations during the transformation would be required to insure appropriate control of the synthetic genes.

If it is contemplated that the recombinant serine protease inhibitors will ultimately be expressed in yeast, it is preferred that the cloning vector first be transferred into Escherichia coli, where the vector would be allowed to replicate and from which the vector would be obtained and purified after

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amplification. The vector would then be transferred into the yeast for ultimate expression of the serine protease inhibitor.

The host microorganisms are cultured under conditions appropriate for the expression of the serine protease inhibitor. These conditions are generally specific for the host organism, and are readily determined by one of ordinary skill in the art, in light of the published literature regarding the growth conditions for such organisms, for example Bergey's Manual of Determinative Bacteriology, 8th Ed., Williams & Wilkins Company, Baltimore, Maryland, which is specifically incorporated herein by reference.

Any conditions necessary for the regulation of the expression of the DNA sequence, dependent upon any operational elements inserted into or present in the vector, would be in effect at the transformation and culturing stages. In one embodiment, the cells are grown to a high density in the presence of appropriate regulatory conditions which inhibit the expression of the DNA sequence. When optimal cell density is approached, the environmental conditions are altered to those appropriate for expression of the synthetic DNA sequence. It is thus contemplated that the production of the protease inhibitor will occur in a time span subsequent to the growth of the host cells to near optimal density, and that the resultant protease inhibitor will be harvested at some time after the regulatory conditions necessary for its expression were induced.

In a preferred embodiment of the present invention, the recombinant protease inhibitor is purified subsequent to harvesting and prior to assumption of its active structure. This embodiment is preferred as the inventors believe that recovery of a high yield of re-folded protein is facilitated if the protein is first purified. However, in one preferred, alternate embodiment, the protease inhibitor may be allowed re-fold to assume its active structure prior to purification. In yet another preferred, alternate embodiment, the protease inhibitor is present in its re-folded, active state upon recovery from the culturing medium.

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In certain circumstances, the protease inhibitor will assume its proper, active structure upon expression in the host microorganism and transport of the protein through the cell wall or membrane or into the periplasmic space. This will generally occur if DNA coding for an appropriate leader sequence has been linked to the DNA coding for the recombinant protein. If the protease inhibitor does not assume its proper, active structure, any disulfide bonds which have formed and/or any noncovalent interactions which have occurred will first be disrupted by denaturing and reducing agents, for example, guanidinium chloride and -mercaptoethanol, before the protease inhibitor is allowed to assume its active structure following dilution and oxidation of these agents under controlled conditions.

It is to be understood that application of the teachings of the present invention to a specific problem or environment will be within the capabilities of one having ordinary skill in the art in light of the teachings contained herein. Examples of the products of the present invention and representative processes for their isolation and manufacture appear in the following example.

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EXAMPLE 1

On the basis of the amino acid sequence described above, the codon usage in highly expressed genes of Escherichia coli, and the provision of convenient restriction endonuclease cleavage sites, the following DNA sequence was proposed:

```

5'AGC  GGT  AAA  HindIII
           AGC  TTC  AAA  GCT  GGC  GTA  TGC  CCG  CCG
           AluI

AAA  AAA  TCC  FnuDII
           GCG  CAG  TGT  CTG  CGG  RsaI  AAA  AAA  HpaII
           HhaI

GAA  TGC  CAG  TCC  GAC  TGG  CAG  TGC  XmaI
           CCG  GGT  AAA  AAA
           HpaII

NciI

CGT  TGT  TGC  NciI
           CCG  GAC  ACC  TGC  GGC  ATC  AAA  TGC  CTG
           HpaII           Fnu4HI           BstNI

BamHI
GAT  CCG  GTT  GAT  ACC  CCG  AAC  CCG  ACT  CGT  CGA  AAA
           HpaII           TagI

NciI
CCG  GGT  AAA  TGC  HpaII
           CCG  GTA  ACC  TAT  BalI
           HpaII           HaeIII

ATG  CTG  AAC  CCG  CCG  AAC  TTC  TGC  GAA  ATG  GAC  GGC
           HaeIII

CAG  TGT  AAA  CGA  BglII
           GAT  CTG  AAA  TGC  TGT  ATG  GGT  ATG
           MboI

Fnu4HI
TGC  GGC  AAA  TCT  TGT  GTT  TCC  NciI
           CCG  GTA  AAA  GCA  TAA 3'
           HpaII

```

To regulate the expression of the protein in a form suitable for export to the periplasm of E. coli, the following regulatory elements were proposed: a tac promoter for initiation of transcription at high levels; a lac operator for transcription regulation; a lac repressor (lac I^q), to be coded elsewhere on the plasmid; an OmpA Shine-Dalgarno sequence to initiate translation at a high level; an OmpA leader to facilitate periplasmic

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export of the product; an Ala of an Ala-Ser junction between the protein sequence encoded by these operator elements and that encoded by the structural genes described above to dictate cleavage of the initial product to yield the mature leukocyte elastase inhibitor. All of these features are incorporated into the following DNA sequence:

CTGCA GCTGT TGACA ATTAA TCATC GGCTC GTCTC GTATA ATGTG ATAAC GAGGC
GCAAA AAATG AAAAA GACAG CTATC GCGAT CGCAG TGGCA
CTGGC TGGTT TCGCT ACCGT AGCGC AGGCC.

To regulate the expression of the protein in a form such that the protein remains in the E. coli cytoplasm, the following operational elements are proposed: the tac promoter; the lac operator, and the lac repressor (lac I^d); a consensus of Shine-Dalgarno sequences; and, to initiate a high level of translation, a fragment of the OmpA leader peptide to be used as a translational coupler. The translational coupling sequence comprises the DNA coding for the translation initiation region of the OmpA gene, the first eight amino acids of the OmpA leader peptide, the consensus Shine-Dalgarno sequence described above and a translational terminator. The translational coupling sequence is to be inserted between the promoter and the translation initiation site of the serine protease inhibitor gene, overlapping the latter. All of these features are incorporated into the following DNA sequence:

CTGCA GCTGT TGACA ATTAA TCATC GGCTC GTCTC GTATA ATGTG ATAAC GAGGC
GCAAA AAATG AAAAA GACAG CTATC GCGAT CGGAG TGTA GAAAT G.

A. Construction of Gene Fragments

To construct the above sequences, the following deoxyribonucleotides are synthesized using the ABI DNA synthesizer (Foster City, California). The products are purified by polyacrylamide gel electrophoresis as described in the ABI instrument manual. They are 5' phosphorylated using T4 polynucleotide kinase and ATP using standard means.

The following group of oligonucleotide sequences are used to construct fragment Aa.

Oligonucleotide Aa1 is:

GCTGT TGACA ATTAA TCAT.

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Oligonucleotide Aa2 is:

CGGCT CGTAT AATGT GTGGA ATTGT GAGCG GATAA CAATT T.

Oligonucleotide Aa3 is:

CACAC ATAAC GAGGC GCAAA AA.

Oligonucleotide Aa4 is:

ATGAA AAAGA CAGCT ATCGC GATCG.

Oligonucleotide Aa5 is:

CAGTG GCACT GGCTG GTTTC GCTAC CGTAG CGCAG GCCAG CGGTA AA.

Oligonucleotide Aa6 is:

GAGCC GATGA TTAAT TGTCA ACAGC TGCA.

Oligonucleotide Aa7 is:

TCCGC TCACA ATTCC ACACA TTATA C.

Oligonucleotide Aa8 is:

CCTCG TTATG TGTGA AATTG TTA.

Oligonucleotide Aa9 is:

GCCAC TCGCA TCGCG ATAGC TGTCT TTTTC ATTTT TTGCG.

Oligonucleotide Aa10 is:

AGCTT TTACC GCTGG CCTGC GCTAC GGTAG CGAAA CCAGC CAGT.

The following oligonucleotide sequences are assembled to make up fragment Ab.

Nucleotide Ab1 is:

GCTGT TGACA ATTAA TCAT.

Nucleotide Ab2 is:

CGGCT CGTAT AATGT GTGGA ATTGT GAGCG GATAA CAATT T.

Nucleotide Ab3 is:

CACAC ATAAC GAGGC GCAAA AA.

Nucleotide Ab4 is:

ATGAA AAAGA CAGCT ATCGC GATCG.

Nucleotide Ab5 is:

GAGTG TAAGA AATGA GCGGT AAA.

Nucleotide Ab6 is:

GAGCC GATGA TTAAT TGTCA ACAGC TGCA.

Nucleotide Ab7 is:

TCCGC TCACA ATTCC ACACA TTATA C.

Nucleotide Ab8 is:

CCTCG TTATG TGTGA AATTG TTA.

Nucleotide Ab9 is:

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AGCTT TTACC GCTCA TTTCT TACAC TCCGA TCGCG ATAGC
TGTCT TTTC ATTTT TTGCG.

The following are the oligonucleotide sequences assembled to construct fragment B.

Oligonucleotide B1 is:

AGCTT CAAAG CTGGC GTATG CCCGC CGAAA AAATC CGCG.

Oligonucleotide B2 is:

CAGTG TCTGC GGTAC AAAAA ACCGG AATGC CAG.

Oligonucleotide B3 is:

TCCGA CTGGC AGTGC CCGGG TAAAA AACGT TGTTG C.

Oligonucleotide B4 is:

CCGGA CACCT GCGGC ATCAA ATGCC TG.

Oligonucleotide B5 is:

GATCC AGGCA TTTGA TGCCG CAGGT GTCCG GGCAA CAACG TTTTT
TACCC GGGCA.

Oligonucleotide B6 is:

CTGCC AGTCG GACTG GCATT CCGGT TTTTT GTACC G.

Oligonucleotide B7 is:

CAGAC ACTGC GCGGA TTTTT TCGGC GGGCA TACGC CAGCT TTGA.

The following are the oligonucleotide sequences used to construct fragment C.

Oligonucleotide C1 is:

GATCC GGTTG ATACC CCGAA CCCG.

Oligonucleotide C2 is:

ACTCG TCGAA AA.

Oligonucleotide C3 is:

CCGGG TAAAT GCCCG GTAAC CTATG GC.

Oligonucleotide C4 is:

CAGTG TCTGA TGCTG AACCC GCCGA AC.

Oligonucleotide C5 is:

TTCTG CGAAA TGGAC GGCCA GTGTA AACGA GAT.

Oligonucleotide C6 is:

CTAGA TCTCG TTTAC ACTGG CCGTC CATTT CGCAG AAGTT.

Oligonucleotide C7 is:

CGGCG GGTTT AGCAT CAGAC ACTGG CCATA GGTTA CCGGG CA.

Oligonucleotide C8 is:

TTTAC CCGGT TTTCG ACGAG TCGGG TT.

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Oligonucleotide C9 is:

CGGGG TATCA ACCG.

The following group of oligonucleotide sequences are assembled to form fragment D.

Oligonucleotide D1 is:

GATCT GAAAT GCTGT ATGGG TATGT GCGGC.

Oligonucleotide D2 is:

AAATC TTGTG TTTCC CCGGT AAAAG CATAA G.

Oligonucleotide D3 is:

TCGAC TTATG CTTTT ACCGG GGAAA CACAA GATTT GCCGC A.

Oligonucleotide D4 is:

CATAC CCATA CAGCA TTTCA.

The following groups of oligonucleotides are mixed and annealed under standard conditions and ligated to each other and to cloning and sequencing vectors M13 mpl8 and 19 cut with appropriate restriction endonucleases using T4 DNA ligase under standard conditions. The products are used to transform E. coli JM105 and clones containing the DNA of interest are selected from white plaques in IPTG- Xgal plates, and further screened by hybridization with ³²P labelled oligonucleotides selected from the group used in the annealing step. The insert structure is confirmed by dideoxy sequencing of the cloned DNA using a universal primer.

Group Aa contains oligonucleotides Aa1-Aa10 which are ligated to M13 mpl8 and 19 cut with PstI and HindIII. Group Ab contains oligonucleotides Ab1-Ab9, which are ligated to M13 mpl8 and 19 cut with PstI and HindIII. Group B, which contains oligonucleotides B1 to B7, is ligated to M13 mpl8 and 19 cut with HindIII and BamHI. Group C, which contains oligonucleotides C1 to C9, is ligated to M13 mpl8 and 19 cut with BamHI and XbaI. Group D, which contains oligonucleotides D1 to D4, is ligated to M13 mpl8 and 19 cut with BamHI and SalI.

M13 replicative form DNA is recovered from the clone having the desired insert DNA by standard means. The insert DNA corresponding to Group Aa is excised from the M13 DNA by cutting the DNA with appropriate restriction endonucleases and is purified by polyacrylamide gel electrophoresis. Its structure is:

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AATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGCTG
GCTCGAGCCATGGGCCCCTAGGAGATCTCAGCTGGACGTCGAC

TTGACAATTAATCATCGGCTCGTATAATGTGTGGAATTGTGAGCG
AACTGTTAATTAGTAGCCGAGCATATTACACACCTTAACACTCGC

GATAACAATTTACACATAACGAGGCGCAAAAA
CTATTGTTAAAGTGTGTATTGCTCCGCGTTTTT

ATGAAAAAGACAGCTATCGCGATCGCAGTGGCACTGGCT
TACTTTTTCTGTCGATAGCGCTAGCGTCACCGTGACCGA

GGTTTCGCTACCGTAGCGCAGGCCAGC
CCAAAGCGATGGCATCGCGTCCGGTCG

GGTAAA
CCATTTTCGA

The insert DNA corresponding to Group Ab is excised by cutting the DNA with restriction endonucleases EcoRI and HindIII and is purified by polyacrylamide gel electrophoresis. Its structure is:

AATTCGAGCTCGGTACCCGGGGATCCTCTA
GCTCGAGCCATGGGCCCCTAGGAGAT

GAGTCGACCTGCAGCTGTTGACAATTAATC
CTCAGCTGGACGTCGACAACTGTTAATTAG

ATCGGCTCGTATAATGTGTGGAATTGTGAG
TAGCCGAGCATATTACACACCTTAACACTC

CGGATAACAATTTACACATAACGAGGCGC
GCCTATTGTTAAAGTGTGTATTGCTCCGCG

AAAAAATGAAAAAGACAGCTATCGCGATCGG
TTTTTTACTTTTTCTGTCGATAGCGCTAGCC

AGTGTAAGAAATGAGCGGTAAA
TCACATTCTTTACTCGCCATTTTCGA

The insert DNA corresponding to Group B is excised by cutting the DNA with restriction endonucleases HindIII and BamHI and is purified by polyacrylamide gel electrophoresis. Its structure is:

AGCTTCAAAGCTGGCGTATGCCCCCGG
AGTTTCGACCGCATACGGGCGGC

AAAAAATCCGCGCAGTGTCTGCGGTACAAA
TTTTTTAGGCGCGTCACAGACGCCATGTTT

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AAACCGGAATGCCAGTCCGACTGGCAGTGC
TTTGGCCTTACGGTCAGGCTGACCGTCACG

CCGGGTAAAAACGTTGTTGCCCCGACACC
GGCCCATTTTTTGCAACAACGGGCCTGTGG

TGCGGCATCAAATGCCTG
ACGCCGTAGTTTACGGACCTAG

The insert DNA corresponding to Group C is excised by cutting the DNA with restriction endonucleases BamHI and BglII and is purified by polyacrylamide gel electrophoresis. Its structure is:

GATCCGGTTGATACCCCGAACCCGACT
GCCAACTATGGGGCTTGGGCTGA

CGTCGAAAACCGGGTAAATGCCCCGTA
GCAGCTTTTGGCCATTTACGGGCCAT

ACCTATGGCCAGTGTCTGATGCTGAACCCG
TGGATACCGGTCACAGACTACGACTTGGGC

CCGAACTTCTGCGAAATGGACGGCCAGTGT
GGCTTGAAGACGCTTTACCTGCCGGTCACA

AAACGA
TTTGCTCTAG

The insert DNA corresponding to Group D is excised by cutting the DNA with restriction endonucleases SauIIIA and SalI and is purified by acrylamide gel electrophoresis. Its structure is:

GATCTGAAATGCTGTATGGGTATG
ACTTTACGACATACCCATAC

TGCGGCAAATCTTGTGTTTCCCCG
ACGCCGTTTAGAACACAAAGGGGC

GTAAAAGCATAAG
CATTTTCGTATTTCAGCT

B. Construction of the Gene

In the construction for export, the inserts from group Aa, B, C, and D are combined and ligated to M13 mpl8 and 19 cut with EcoRI and SalI using T4 DNA ligases under standard conditions. The clones containing the gene are selected by their color on Xgal plates and screened further by hybridization with the ³²P labelled oligonucleotide. The structure of selected

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clones is confirmed by dideoxy sequencing of the insert region of the DNA using the universal primer.

In the construction for cytoplasmic expression, the inserts from groups Ab, B, C, and D are combined and ligated to M13 mp18 and 19 cut with EcoRI and SalI using T4 DNA ligase under standard conditions. The clones containing the genes are selected by their color on Xgal plates and screened further by hybridization with the ³²P labelled insert. The structures of selected clones are confirmed by dideoxy sequencing of the insert region of the DNA using the universal primer.

EXAMPLE 2

On the basis of the amino acid sequence described above, the codon usage in highly expressed genes of Escherichia coli, and the provision of convenient restriction endonuclease cleavage sites, the following DNA sequence was proposed:

```

5'TCT GGT AAA HindIII
               AGC TTC
               AluI
AAA AAA FnuDII
      TCC GCG CAG TGT CTG CCG RsaI AAA AAA HpaII
               HhaI          TAC          CCG

GAA TGC CAG TCC GAC TGG CAG TGC XmaI
               CCG GGT AAA AAA
               HpaII

NciI

CGT TGT TGC HpaII
      CCG GAC ACC TGC GGC ATC AAA TGC CTG
      NciI          Fnu4HI          BstNI

BamHI
GAT CCG GTT GAT ACC CCG AAC CCG ACT CGT CGA AAA
      HpaII          TaqI

HpaII
CCG GGT AAA TGC HpaII
      NciI          CCG GTA ACC TAT BalI
               NciI          GGC CAG TGT CTG
               HaeIII

ATG CTG AAC CCG CCG AAC TTC TGC GAA ATG GAC GGC
               HaeIII

CAG TGT AAA CGA BglII
      GAT CTG
      MboI

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$\frac{\text{Fnu4HI}}{\text{TGC GGC}}$ AAA TCT TGT GTT TCC $\frac{\text{NciI}}{\text{CCG GTA}}$ AAA GCA TAA 3'

GAATT CGATA TCTCG TTGGA GATAT TCAT GACGT ATTTT GGATG ATAAC GAGGC
GCAAA AAATG AAAAA GACAG CTATC GCGAT CGCAG TGGCA
CTGGC TGGTT TCGCT ACCGT AGCGC AGGCC.

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GAATT CGATA TCTCG TTGGA GATAT TTCAT GACGT ATTTT GGATG ATAAC GAGGC
GCAAA AAATG AAAAA GACAG CTATC GCGAT CAAGG AGAAA TAAAT G.

C. Construction of Gene Fragments

To construct the above sequences, the following deoxy-ribonucleotides are synthesized using the ABI DNA synthesizer (Foster City, California). The products are purified by polyacrylamide gel electrophoresis as described in the ABI instrument manual. They are 5' phosphorylated using T4 polynucleotide kinase and ATP using standard means.

The following group of oligonucleotide sequences are used to construct fragment Aa.

Oligonucleotide Aa1 is:

AATTTCGATATCTCGTTGGAGATATTCATGACGTATTTTGGATGATAACGAGGCGCAAAA.

Oligonucleotide Aa2 is:

ATGAAAAAGACAGCTATCGCGATCG.

Oligonucleotide Aa3 is:

GATCCGATCGCGATAGCTGTCTTTTTCATTTTTTGC.

Oligonucleotide Aa4 is:

GCCTCGTTATCATCCAAAATACGTATGAATATCTCCAACGAGATATCG.

Oligonucleotide Aa5 is:

GATCCGATCGCAGTGGCACTGGCTGGTTTCGCTACCGTAGCGCAGGCCTCTGGTAAA.

Oligonucleotide Aa6 is:

AGCTTTTACCAGAGGCCTGCGCTACGGTAGCGAAACCAGCCAGTGCCACTGCGATCG.

The following oligonucleotide sequences are assembled to make up fragment Ab.

Oligonucleotide Ab1 is:

AATTTCGATATCTCGTTGGAGATATTCATGACGTATTTTGGATGATAACGAGGCGCAAAA.

Oligonucleotide Ab2 is:

ATGAAAAAGACAGCTATCGCGATCG.

Oligonucleotide Ab3 is:

GATCCGATCGCGATAGCTGTCTTTTTCATTTTTTGC.

Oligonucleotide Ab4 is:

GCCTCGTTATCATCCAAAATACGTATGAATATCTCCAACGAGATATCG.

Oligonucleotide Ab5 is:

CAAGGAGAAATAAATGAGCGGTAAA.

Oligonucleotide Ab6 is:

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AGCTTTTACCGCTCATTTATTTCTCCTTGAT.

The following are the oligonucleotide sequences assembled to construct fragment B.

Oligonucleotide B1 is:

AGCTT CAAAG CTGGC GTATG CCCGC CGAAA AAATC CGCG.

Oligonucleotide B2 is:

CAGTG TCTGC GGTAC AAAAA ACCGG AATGC CAG.

Oligonucleotide B3 is:

TCCGA CTGGC AGTGC CCGGG TAAAA AACGT TGTTG C.

Oligonucleotide B4 is:

CCGGA CACCT GCGGC ATCAA ATGCC TG.

Oligonucleotide B5 is:

GATCC AGGCA TTTGA TGCCG CAGGT GTCCG GGCAA CAACG TTTTT
TACCC GGGCA.

Oligonucleotide B6 is:

CTGCC AGTCG GACTG GCATT CCGGT TTTTT GTACC G.

Oligonucleotide B7 is:

CAGAC ACTGC GCGGA TTTTT TCGGC GGGCA TACGC CAGCT TTGA.

The following are the oligonucleotide sequences used to construct fragment C.

Oligonucleotide C1 is:

GATCC GGTTC ATACC CCGAA CCCG.

Oligonucleotide C2 is:

ACTCG TCGAA AA.

Oligonucleotide C3 is:

CCGGG TAAAT GCCCG GTAAC CTATG GC.

Oligonucleotide C4 is:

CAGTG TCTGA TGCTG AACCC GCCGA AC.

Oligonucleotide C5 is:

TTCTG CGAAA TGGAC GGCCA GTGTA AACGA GAT.

Oligonucleotide C6 is:

CTAGA TCTCG TTTAC ACTGG CCGTC CATTT CGCAG AAGTT.

Oligonucleotide C7 is:

CGGCG GGTTC AGCAT CAGAC ACTGG CCATA GGTTA CCGGG CA.

Oligonucleotide C8 is:

TTTAC CCGGT TTTCG ACGAG TCGGG TT.

Oligonucleotide C9 is:

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CGGGG TATCA ACCG.

The following group of oligonucleotide sequences are assembled to form fragment D.

Oligonucleotide D1 is:

GATCT GAAAT GCTGT ATGGG TATGT GCGGC.

Oligonucleotide D2 is:

AAATC TTGTG TTTCC CCGGT AAAAG CATAA G.

Oligonucleotide D3 is:

TCGAC TTATG CTTTT ACCGG GGAAA CACAA GATTT GCCGC A.

Oligonucleotide D4 is:

CATAC CCATA CAGCA TTTCA.

The following groups of oligonucleotides are mixed and annealed under standard conditions and ligated to each other and to cloning and sequencing vectors M13 mp18 and 19 cut with appropriate restriction endonucleases using T4 DNA ligase under standard conditions. The products are used to transform E. coli JM105 and clones containing the DNA of interest are selected by hybridization with ³²P labelled oligonucleotides selected from the group used in the annealing step. The insert structure is confirmed by dideoxy sequencing of the cloned DNA using a universal primer.

Oligonucleotides Aa1-Aa4 are ligated to M13mp18 and M13mp19 cut with EcoRI and BamHI. M13 replicative form DNA having the desired insert DNA is recovered by standard means. The insert DNA is excised from the M13 DNA by cutting the M13 DNA with restriction endonucleases EcoRI and PvuI and is purified by polyacrylamide gel electrophoresis. Its structure is:

AATTCGATATCTCGTTGGAGATATTCATGACGTATTTTGGATGATAACGAGGCGCAAAAAATGA
GCTATAGAGCAACCTCTATAAGTACTGCATAAAACCTACTATTGCTCCGCGTTTTTACT
AAAAGACAGCTATCGCGAT
TTTTCTGTGCGATAGCGC

Oligonucleotides Aa5 and Aa6 are ligated to M13mp18 and m13mp19 cut with BamHI and HindIII. M13 replicative form DNA having the desired insert DNA is recovered by standard means. The insert DNA is excised from the M13 DNA by cutting the DNA with restriction endonucleases PvuI and HindIII and is purified by polyacrylamide gel electrophoresis. Its structure is:

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CGCAGTGGCACTGGCTGGTTTCGCTACCGTAGCGCAGGCCTCTGGTAAA
TAGCGTCACCGTGACCGACCAAAGCGATGGCATCGCGTCCGGAGACCATTTTCGA
This PvuI-HindIII fragment is combined with the EcoRI-PvuI fragment prepared from oligonucleotides Aa1-Aa4 and ligated with M13mpl8 or M13mpl9 cut with EcoRI and HindIII. M13 replicative form DNA having the desired insert DNA is recovered by standard means. The insert DNA, which is DNA Fragment Aa, is excised from the M13 DNA by cutting the M13 DNA with restriction endonucleases EcoRI and HindIII and is purified by polyacrylamide gel electrophoresis. Its structure is:

AATTCGATATCTCGTTGGAGATATTCATGACGTATTTTGGATGATAACGAGGCGCAAAAAATGA
GCTATAGAGCAACCTCTATAAGTACTGCATAAAACCTACTATTGCTCCGCGTTTTTTACT
AAAAGACAGCTATCGCGATCGCAGTGGCACTGGCTGGTTTCGCTACCGTAGCGCAGGCCTCTGGTA
TTTTCTGTGCTAGCGCTAGCGTCACCGTGACCGACCAAAGCGATGGCATCGCGTCCGGAGACCAT
AA
TTTCGA

Oligonucleotides Ab1-Ab4 are ligated to M13mpl8 and M13mpl9 cut with EcoRI and BamHI. M13 replicative form DNA having the desired insert DNA is recovered by standard means. The insert DNA is excised from the M13 DNA by cutting the DNA with restriction endonucleases EcoRI and PvuI and is purified by polyacrylamide gel electrophoresis. Its structure is:

AATTCGATATCTCGTTGGAGATATTCATGACGTATTTTGGATGATAACGAGGCGCAAAAAATGA
GCTATAGAGCAACCTCTATAAGTACTGCATAAAACCTACTATTGCTCCGCGTTTTTTACT
AAAAGACAGCTATCGCGAT
TTTTCTGTGCTAGCGC

This EcoRI-PvuI fragment is combined with oligonucleotides Ab5 and Ab6 and ligated with M13mpl8 or M13mpl9 cut with EcoRI and HindIII. M13 replicative form DNA having the desired insert DNA is recovered by standard means. The insert DNA which is Fragment Ab is excised from the M13 DNA by cutting the DNA with restriction endonucleases EcoRI and HindIII and is purified by polyacrylamide gel electrophoresis. Its structure is:

AATTCGATATCTCGTTGGAGATATTCATGACGTATTTTGGATGATAACGAGGCGCAAAAAATGA
GCTATAGAGCAACCTCTATAAGTACTGCATAAAACCTACTATTGCTCCGCGTTTTTTACT
AAAAGACAGCTATCGCGATCAAGGAGAAATAAATGAGCGGTAAA
TTTTCTGTGCTAGCGCTAGTTCCTCTTTATTTACTCGCCATTTTCGA

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Group B, which contains oligonucleotides B1 to B7, is ligated to M13mp 18 and 19 cut with HindIII and BamHI. The insert DNA corresponding to Group B is excised by cutting the DNA with restriction endonucleases HindIII and BamHI and is purified by polyacrylamide gel electrophoresis. Its structure is:

AGCTTCAAAGCTGGCGTATGCCCCGCG

AGTTTCGACCGCATACGGGCGGC

AAAAAATCCGCGCAGTGTCTGCGGTACAAA

TTTTTTTAGGCGCGTCACAGACGCCATGTTT

AAACCGGAATGCCAGTCCGACTGGCAGTGC

TTTGGCCTTACGGTCAGGCTGACCGTCACG

CCGGGTAAAAAACGTTGTTGCCCGGACACC

GGCCCATTTTTTGCAACAACGGGCCTGTGG

TGCGGCATCAAATGCCTG

ACGCCGTAGTTTACGGACCTAG

Group C, which contains oligonucleotides C1 to C9, is ligated to M13mp 18 and 19 cut with BamHI and XbaI. The insert DNA corresponding to Group C is excised by cutting the DNA with restriction endonucleases BamHI and BglII and is purified by polyacrylamide gel electrophoresis. Its structure is:

GATCCGGTTGATACCCCGAACCCGACT

GCCAACTATGGGGCTTGGGCTGA

CGTCGAAAACCGGGTAAATGCCCGGTA

GCAGCTTTTGGCCCATTTACGGGCCAT

ACCTATGGCCAGTGTCTGATGCTGAACCCG

TGGATACCGGTCACAGACTACGACTTGGGC

CCGAACTTCTGCGAAATGGACGGCCAGTGT

GGCTTGAAGACGCTTTACCTGCCGGTCACA

AAACGA

TTTGCTCTAG

Group D, which contains oligonucleotides D1 to D4, is ligated to M13mp 18 and 19 cut with BamHI and SalI. The insert DNA corresponding to Group D is excised by cutting the DNA with restriction endonucleases SauIIIA and SalI and is purified by acrylamide gel electrophoresis. Its structure is:

GATCTGAAATGCTGTATGGGTATG

ACTTTACGACATACCCATAC

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TGCGGCAAATCTTGTGTTTCCCCG
ACGCCGTTTAGAACACAAAGGGGC
GTAAAAGCATAAG
CATTTTCGTATTTCAGCT

D. Construction of the Gene

In the construction for export, the inserts from Groups Aa, B, C, and D are combined and ligated to M13 mp18 and 19 cut with EcoRI and SalI using T4 DNA ligase under standard conditions. In the construction for cytoplasmic expression, the inserts from Groups Ab, B, C and D are combined and ligated to M13 mp18 and 19 cut with EcoRI and SalI using T4 DNA ligase under standard conditions. The clones containing the gene are selected by their color on Xgal plates and screened further by hybridization with the ³²P labelled oligonucleotide. The structure of selected clones is confirmed by dideoxy sequencing of the insert region of the DNA using the universal primer.

EXAMPLE 3

Construction of Expression Vectors

The inserts for the construction for export and the construction for cytoplasmic expression were transferred to expression plasmids as follows. M13 replicative form DNA having the desired insert DNA is recovered by standard means as indicated above. The appropriate insert DNA is excised from the M13 DNA by cutting the DNA with restriction endonucleases EcoRI and PstI and is purified by polyacrylamide gel electrophoresis. It is then ligated to pKK223-3 cut with restriction endonucleases EcoRI and PstI and the resulting plasmid cloned into E. coli JM107. The construction for use in Examples 4 and 5 for export is pSGE6 and that for use in Example 7 for cytoplasmic expression is pSGE8. The E. coli strain for export in Examples 4 and 5 is SGE10 and that for cytoplasmic expression in Example 6 is SGE30.

A. Organization of pSGE6

Plasmid pSGE6 was constructed by replacing the DNA between the EcoRI and PstI sites of pKK223-3 with an EcoRI/PstI fragment containing DNA coding for ompA SLPI. The DNA sequence of ompA-SLPI is as follows:

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      10           20           30           40           50           60
GAATTCGATA TCTCGTTGGA GATATTCATG ACGTATTTTG GATGATAACG AGGCGCAAAA
CTTAAGCTAT AGAGCAACCT CTATAAGTAC TGCATAAAAC CTACTATTGC TCCGCGTTTT

      70           80           90          100          110          120
AATGAAAAAG ACAGCTATCG CGATCGCAGT GGCAGTGGCT GGTTCGCTA CCGTAGCGCA
TTACTTTTTC TGTCGATAGC GCTAGCGTCA CCGTGACCBA CCAAAGCGAT GGCATCGCGT

      130          140          150          160          170          180
GGCCTCTGGT AAAAGCTTCA AAGCTGGCGT ATGCCC GCCG AAAAAATCCG CGCAGTGTCT
CCGGAGACCA TTTTCGAAGT TTCGACCGCA TACGGGCGGC TTTT TTAGGC GCGTCACAGA

      190          200          210          220          230          240
GCGGTACAAA AAACCGGAAT GCCAGTCCGA CTGGCAGTGC CCGGGTAAAA AACGTTGTTG
CGCCATGTTT TTTGGCCTTA CGGTCAGGCT GACCGTCACG GGCCCATTTT TTGCAACAAC

      250          260          270          280          290          300
CCCGGACACC TCGGGCATCA AATGCCTGGA TCCGGTTGAT ACCCCGAACC CGACTCGTCG
GGGCCTGTGG ACGCCGTAGT TTACGGACCT AGGCCAACTA TGGGGCTTGG GCTGAGCAGC

      310          320          330          340          350          360
AAAACCGGGT AAATGCCCGG TAACCTATGG CCAGTGTCTG ATGCTGAACC CGCCGAAC TT
TTTTGGCCCA TTTACGGGCC ATTGGATACC GGTACAGAC TACGACTTGG GCGGCTTGAA

      370          380          390          400          410          420
CTGCGAAATG GACGGCCAGT GTAAACGAGA TCTGAAATGC TGTATGGGTA TGTGCGGCAA
GACGCTTTAC CTGCCGGTCA CATTGTCTCT AGACTTTACG ACATACCCAT ACACGCCGTT

      430          440          450          460
ATCTTGTTGT TCCCCGGTAA AAGCATAAGT CGACCTGCAG
TAGAACACAA AGGGGCCATT TTCGTATTCA GCTGGACGTC

```

The sequence hereinafter referred to as "ompA-SLPI" is the DNA from the final M13mpl8 construct for export discussed above. Plasmid pSGE6 is depicted in Figure 1. In Fig. 1, the first codon for ompAss-SLPI is at position 62-64 of the DNA sequence called "ompA-SLPI." The first codon for mature SLPI is at position 125-127. Ptac contains DNA for the tac promoter, lac operator and the beta galactosidase Shine/Dalgarno sequence. The abbreviations R1, Pst and Bam are recognition sequences for the restriction enzymes EcoRI, PstI and BamHI. Tet^r is a part of the gene from pBR322 which confers resistance to tetracycline, amp^r confers resistance to ampicillin, rrnB contains the DNA from the rrnB operon from position 6416 to position 6840. Arrows indicate the direction of transcription.

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B. Organization of pCJ-ompA-SLPI

Plasmid pCJ-ompA-SLPI is the same as pSGE6 except that it contains the complete tetracycline resistance gene and promoter rather than the partial gene. This plasmid confers tetracycline resistance when inserted into E. coli and was constructed in a analogous fashion to pSGE6 except that the EcoRI/PstI fragment containing DNA coding for ompA SLPI was cloned into vector pCJ1 rather than pKK223-3. The vector pCJ1 was constructed as follows. Plasmid pKK223-3 was digested completely with SphI and partially with BamHI. A 4.4Kbp fragment was gel purified and combined with a synthetic adaptor:

GATCTAGAATTGTCATGTTTGACAGCTTATCAT

ATCTTAACAGTACAAACTGTCTGAATAGTAGC

and a 539 bp fragment of DNA from a ClaI, SphI digest of the tet^r gene of pBR322 (PL Biochemicals, 27-4891-01).

C. Structure of pSGE8

Plasmid pSGE8 is isogenic to pSGE6 with the exception that the DNA between the EcoRI and Pst sites contains the sequence called ompA-tc-met-SLPI which is derived from the final M13mpl8 construct for cytoplasmic expression as discussed above. This sequence directs the synthesis of methionyl-SLPI in the cytoplasm of E. coli. A partial diagram of pSGE8 is contained in Fig. 2. In the sequence called "ompA-tc-met-SLPI," the initiation codon for ompA is at position 62-64, the termination codon is at 95-97, and the initiation codon for methionyl-SLPI is at 98-100. The DNA sequence of ompA-tc-met-SLPI is as follows:

10	20	30	40	50	60
GAATTCGATA	TCTCGTTGGA	GATATTCATG	ACGTATTTTG	GATGATAACG	AGGCGCAAAA
CTTAAGCTAT	AGAGCAACCT	CTATAAGTAC	TGCATAAAAC	CTACTATTGC	TCCGCGTTTT
70	80	90	100	110	120
AATGAAAAAG	ACAGCTATCG	CGATCAAGGA	GAAATAAATG	AGCGGTAAAA	GCTTCAAAGC
TTACTTTTTT	TGTCGATAGC	GCTAGTTCCT	CTTTATTTAC	TCGCCATTTT	CGAAGTTTCG
130	140	150	160	170	180
TGGCGTATGC	CCGCCGAAAA	AATCCGCGCA	GTGTCTGCGG	TACAAAAAAC	CGGAATGCCA
ACCGCATACG	GGCGGCTTTT	TTAGGCGCGT	CACAGACGCC	ATGTTTTTTG	GCCTTACGGT
190	200	210	220	230	240
GTCCGACTGG	CAGTGCCCGG	GTAAAAACG	TTGTTGCCCG	GACACCTGCG	GCATCAAATG
CAGGCTGACC	GTCACGGGCC	CATTTTTTGC	AACAACGGGC	CTGTGGACGC	CGTAGTTTAC

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      250      260      270      280      290      300
CCTGGATCCG GTTGATACCC CGAACCCGAC TCGTCGAAAA CCGGGTAAAT GCCCGGTAAC
GGACCTAGGC CAACTATGGG GCTTGGGCTG AGCAGCTTTT GGCCCATTTA CGGGCCATTG

      310      320      330      340      350      360
CTATGGCCAG TGTCTGATGC TGAACCCGCC GAACTTCTGC GAAATGGACG GCCAGTGTA
GATACCGGTC ACAGACTACG ACTTGGGCGG CTTGAAGACG CTTTACCTGC CGGTCACATT

      370      380      390      400      410      420
ACGAGATCTG AAATGCTGTA TGGGTATGTG CGGCAAATCT TGTGTTTCCC CGGTAAAAGC
TGCTCTAGAC TTTACGACAT ACCCATAAC GCGGTTTAGA ACACAAAGGG GCCATTTTCG

      430
ATAAGTCGAC CTGCAG
TATTCAGCTG GACGTC

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D. Organization of pCJ-met-SLPI

Plasmid pCJ-met-SLPI is the same as pSGE8 except that it contains the complete (rather than the partial) tetracycline resistance gene. Plasmid CJ-met-SLPI was constructed analogously to pSGE8 except that the EcoRI/PstI fragment containing DNA coding for ompA-tc-met-SLPI was cloned into vector pCJ1 rather than pKK223-3.

E. Construction of Yeast Expression Plasmids

The plasmid pUC8 was digested with HindIII and ligated to a HindIII/SmaI adaptor (obtained from Amersham, Cat. No. DA1006). The addition of this adaptor to a HindIII site does not reconstruct the HindIII site. The DNA was then digested with SmaI and ligated in dilute solution followed by transformation of E. coli JM83. The correct plasmid, i.e., a plasmid lacking the restriction sites in the polylinker from the HindIII site to the SmaI site, was identified by digesting plasmid DNA isolated from transformants with EcoRI, SmaI or HindIII. A transformant containing a plasmid that lacked the HindIII site but contained the EcoRI site and SmaI site was identified in this manner. This plasmid is pGS185.

An EcoRI fragment containing the yeast MF 1 gene was purified by gel electrophoresis from the plasmid pCY17 as described by J. Kurjan & I. Herskowitz in Cell 30:933 (1982), specifically incorporated herein by reference, and ligated into EcoRI cut pGS185. This ligation mixture was used to transform E. coli HB101, selecting for ampicillin resistance. Plasmid DNA was

isolated from transformants and the presence of the correct insert confirmed by digests of the DNA with EcoRI. This is plasmid pGS285 and is depicted in Fig. 3.

Plasmid pGS285 was digested to completion with HindIII and religated under dilute conditions to eliminate three of the four internal HindIII sites in the MF 1 gene as noted by Kurjan & Herskowitz, ibid. The correct construct was selected as described above. This is plasmid pGS385.

The M13 AaBCD clone as described in Example 2 that carries nucleotide sequences encoding amino acids four through 107 of the synthetic SLPI gene, was digested with HindIII. This DNA was ligated with the following oligonucleotide adaptor:

5' GCT GAA GCT TCA GGT AAG

CGA CTT CGA AGT CCA TTC TCGA.

This adaptor had been formed by annealing the two oligonucleotides:

5' GCT GAA GCT TCA GGT AAG and 5' AGC TCT TAC CTG AAG CTT CAGC first at 70°C for 2' followed by slow cooling overnight.

Following ligation of the adaptor to HindIII cut M13 AaBCD, the ligation mix was digested with HindIII and SalI to release a fragment purified by agarose gel electrophoresis and electrolution. This fragment was digested once more with HindIII and then ligated with pGS385 DNA that had been cut with HindIII and SalI. E. coli HB101 was transformed with the ligation mixture and ampicillin resistant transformants were selected. Transformants containing plasmids with the correct insert DNA were identified by preparing plasmid DNA and digesting it with HindIII and SalI. A plasmid constructed and isolated in this manner has been designated pGS485 and is depicted in Figure 4. This plasmid contains the MF 1 gene fused, in frame, to the synthetic SLPI gene at the HindIII site in the first spacer region of the MF 1 gene. Such constructs, when placed in yeast, have been demonstrated to direct the synthesis, processing and secretion of the heterologous proteins as shown by A.J. Brake et al. in PNAS (USA) 81:4642, specifically incorporated herein by reference. The fusion of the MF 1 gene and SLPI is contained on an EcoRI fragment in pGS485. This EcoRI fragment was cloned into the vector YIp5 as described in Example 8.

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EXAMPLE 4

Expression and purification of secretory leukocyte protease inhibitor (SLPI) using plasmid pSGE6.

E. coli cells containing plasmid pSGE6 (SGE10 cells) were cultured for 6 hours in 10 liters of M9 media with 2% tryptone, 0.5% yeast extract, 20g/l glucose, 200 mg/l Vitamin B₁ and 100 mg/l ampicillin added. IPTG was added to 0.2mM and the culture grown for another 6 hours. Ten liters of E. coli SGE10 cells, at 8 grams per liter, were pelleted at 18,000 x g and resuspended in 50mM Tris.HCl (pH 7.5), 4mM EDTA buffer (hereinafter T50E4) and pelleted. The pellet was resuspended in 2.7 liters T50E4 and frozen in 150ml lots. Eight of these lots (equivalent to 36 gms of cells) were pooled and lysed by a single pass through a french press at 12,000 psi and 4° C. The lysate was centrifuged for 1.5hrs at 20,000 x g. One sixth of the pellet containing the cell insolubles (equivalent to six grams of cells) was washed twice with 125ml of T50E4 and the remaining material was frozen overnight.

The frozen pellet was extracted with 25ml of 100mM Tris.HCl (pH 8.0), 4mM EDTA (hereinafter T100E4) containing 20mM DTT (obtained from Sigma, Cat. No. D-0632), 4mM PMSF (obtained from Sigma, Cat. No. P-7626) and 8M urea (ultrapure, obtained from BRL, Cat. No. 5505UA) for 1hr at 37° C. and centrifuged at 10,000 x g for ten minutes. The resultant supernatant was mixed with 10ml packed Sephadex SP-C25 (obtained from Pharmacia) which had been pre-equilibrated with the extraction buffer T100E4 containing 20mM DTT and 8M urea and mixed on a roller for ten minutes at 37°C to absorb the SLPI to the SP-Sephadex.

The resin with the absorbed SLPI was pelleted by a ten minute centrifuge at 3,000 x g and the supernatant decanted. The remaining resin was washed twice with 25ml of T100E4 containing 20mM DTT and 8M urea followed by two washes with 25ml T100E4 containing 20mM DTT. The resin was then extracted once with a mixture of 0.6ml 5 M NaCl and 25ml of T100E4 containing 20 mM DTT and 0.3 M NaCl. This extract contained about 0.15mg/ml protein and more than 0.04mg/ml SLPI. The SLPI obtained by this method was determined to be greater than 70% pure by high pressure liquid chromatography.

EXAMPLE 5

Using the method of Example 4, a second frozen pellet was extracted with T100E4 containing 1% Triton x-100 (obtained from Sigma, Cat. No. T-6878) in place of the first T100E4/DTT/PMSF/urea wash. The resultant SLPI was slightly more pure than that obtained in Example 4 and gave higher activity in the refolding assay set forth in Example 6 below.

EXAMPLE 6

Refolding purified SLPI.

About 40ug of partially-purified SLPI from Example 4 or 5 was made 8M in urea or 5M in guanidine hydrochloride (obtained from Pierce Chemical Co., #24110), and 4mM in DTT and incubated for 1hr at room temperature. Oxidized glutathione (obtained from Sigma, Cat. No. G-4626) was added to 13.5mM and the mixture was again incubated for 1 hr at room temperature. The mixture was diluted 10-fold with a solution of 50mM Tris in NaOH, pH10.7 and incubated for a further 4 hrs at room temp. The mixture was then diluted 5-fold with 50mM Tris, pH8.0, and 0.15M NaCl and applied to a 1 x 2 cm column of Sephadex SP-C25 preequilibrated with 50mM Tris, pH8.0 and 0.25M NaCl. The resin was washed with 50mM Tris, pH 8.0, containing 0.25M NaCl and then with 50mM Tris, pH8.0, containing 0.5M NaCl. The fraction eluting with the 0.5M salt wash was fully active and represented about 30% of the SLPI applied to the column.

EXAMPLE 7

Purification of SLPI from soluble and insoluble fractions of SGE30 cell lysate.

Expression of the plasmid pSGE8 in E. coli SGE30 cells produced SLPI in both the soluble and insoluble fractions of the cell lysate. At 1% of the total cell protein, the SLPI was distributed about 80% to the soluble and about 20% to the insoluble fractions.

A. Purification of SLPI from the insoluble fraction

The E. coli SGE30 cells containing pSGE8 were grown in LB Media containing 50 ug/ml ampicillin in a shaker flask to an OD600 of 0.7 and induced by the addition of IPTG to 0.2mM. After three hours the cells are pelleted and were suspended in two

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A. Purification of SLPI from the insoluble fraction

The E. coli SGE30 cells containing pSGE8 were grown in LB Media containing 50 ug/ml ampicillin in a shaker flask to an OD600 of 0.7 and induced by the addition of IPTG to 0.2mM. After three hours the cells are pelleted and were suspended in two times their weight of 50mM Tris.HCl (pH 7.5) and 4mM EDTA (hereinafter T50E4). The cells were disrupted by sonication at 4° C. and the extract was centrifuged for 20 minutes at 4° C. at 12,000 x g.

The pellet was washed in three volumes of T50E4 and was solublized at room temperature in a solution containing either 10M urea or 6M guanidine hydrochloride, and 5mM reduced DTT. After a one hour incubation at room temperature, oxidized glutathione was added at a concentration of 17.5mM and the mixture was incubated for another hour. The mixture was then diluted into 10 volumes of 50 mM Tris.HCl, pH 10.7. The diluted mixture was allowed to stand for 4 hours at room temperature followed by pH adjustment to 8 by the addition of 5 N HCl. This mixture was centrifuged to remove precipitated protein.

The supernatant so produced contained SLPI which exhibited secretory leukocyte protease inhibitor activity. This protein was purified by chromatography on a Sephadex SP-C25 column as described above.

B. Purification of SLPI from soluble fraction

E. coli SGE30 cells containing plasmid pSGE8 were grown in a shaker flask to an OD600 of 0.7 and induced by the addition of IPTG to 0.2mM. At an OD600 of 1.1, the cells were pelleted at 25,000 x g for 15 minutes. The pellet was resuspended in T50E4 and was lysed by two passages through a french press at 20,000 psi at 4° C. The lysate was centrifuged at 25,000 x g for 15 minutes.

The supernatant was made 25mM in DTT. This mixture was incubated at 0° C. for one hour and sufficient HCl was added to reach a final concentration of 5%. After a 30 minute incubation at 0° C., the mixture was centrifuged at 25,000 x g for 15 minutes and the supernatant removed for further processing. The pH of the supernatant was adjusted to 8.0 with 10M NaOH and

EXAMPLE 8

The EcoRI fragment containing the fused SLPI-MF 1 gene (see Ex. 3.E.) was ligated to the EcoRI site of the yeast vector YIp5 as described by D. Botstein and R.W. Davis in The Molecular Biology of the Yeast Saccharomyces, Cold Spring Harbor Laboratory, pp. 607-636 (1982), specifically incorporated herein by reference, to generate YIpSLPI-1 and has been integrated into the URA3 gene of S. cerevisiae BS214 (MAT , Ura3-52, pep4, prb1) by site-directed recombination as described by T. Orr-Weaver et al. in Methods in Enzymology 101:228 (1983), specifically incorporated herein by reference. This strain, S. cerevisiae SGY-1, secretes fully active SLPI into the culture supernate.

A second strain, SGY-3, also produces and secretes active SLPI. This strain carries the MF 1::SLPI fusion on the replicating yeast plasmid pGS585. This plasmid was constructed from pJDB207 as described by J.R. Broach in Methods in Enzymology 101:307 (1983), specifically incorporated herein by reference, by the addition of the yeast URA3 gene, isolated from the plasmid YEp24 as described by D. Botstein and R.W. Davis in The Molecular Biology of the Yeast Saccharomyces, Cold Spring Harbor Laboratory, pp. 607-636, specifically incorporated herein by reference, and cloned into the HindIII site of pJDB207 to construct pGS585. The MF 1::SLPI fusion gene, contained on an EcoRI fragment, was cloned into the Sall site of pGS585 using EcoRI-XhoI adaptors (obtained from Amersham, Cat. No. DA1007) to generate YEpSLPI-1. This plasmid was introduced into S. cerevisiae DBY746 (MAT , Ura3-52, leu2-3, his3 1, trp 1-289) by transformation as described by Ito et al. in J. Bacteriology 153:163 (1983), specifically incorporated herein by reference.

Saccharomyces cerevisiae strains SGY-1 and SGY-3 were grown at 30°C to stationary phase in SD medium lacking uracil according to the method of F. Sherman et al. described in Methods in Yeast Genetics, p. 62, Cold Spring Harbor Laboratories, Cold Spring Harbor, New York (1981), specifically incorporated herein by reference. Cells were removed from the culture medium by centrifugation and the culture supernatant was assayed for SLPI activity by measuring (1) protease inhibitory activity and (2)

the amount of material that specifically reacts with anti-SLPI antibodies by an enzyme-linked immunoassay. Purification schemes may be developed in a manner analogous to prior methods described herein.

It will be apparent to those skilled in the art that various modifications and variations can be made to the processes and products of the present invention. Thus, it is intended that the present invention cover the modifications and variations of this invention provided they come within the scope of the appended claims and their equivalents.

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WHAT IS CLAIMED IS:

1. A method for the recombinant DNA synthesis of a single polypeptide chain serine protease inhibitor having at least one active site possessing serine protease inhibitor activity comprising:

(a) Preparation of a DNA sequence capable of directing a host microorganism to produce a protein having serine protease inhibitor activity, said inhibitor exhibiting substantial homology to the native serine protease inhibitor isolated from parotid secretions;

(b) Cloning the DNA sequence into a vector capable of being transferred into and replicating in a host microorganism, such vector containing operational elements for the DNA sequence;

(c) Transferring the vector containing the DNA sequence and operational elements into a host microorganism capable of expressing the protease inhibiting protein;

(d) Culturing the host microorganism under conditions appropriate for amplification of the vector and expression of the inhibitor;

(e) Harvesting the inhibitor; and

(f) Permitting the inhibitor to assume an active tertiary structure whereby it possesses serine protease inhibitor activity.

2. The method of claim 1 wherein said DNA sequence is a synthetic sequence.

3. The method of claim 1 wherein said DNA sequence is a natural DNA sequence.

4. The method of claim 1 wherein said method further comprises purification of the inhibitor.

5. The method of claim 4 wherein said purification is conducted prior to permitting said inhibitor to assume an active form.

6. The method of claim 4 wherein said purification is conducted subsequent to permitting said inhibitor to assume an active form.

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7. The method of claim 1 wherein said vector is constructed from parts of the vectors selected from the group consisting of pBR322 and pIQ.

8. The method of claim 1 wherein said host microorganism is selected from the group consisting of microorganisms of the genera Escherichia, Bacillus and Saccharomyces.

9. The method of claim 8 wherein said host microorganism is Escherichia coli.

10. The method of claim 8 wherein said host microorganism is Bacillus subtilis.

11. The method of claim 8 wherein said host microorganism is Saccharomyces cerevisiae.

12. The method of claim 3 wherein said natural DNA sequence is obtained by the method comprising:

(a) Preparation of a human cDNA library from cells capable of generating a serine protease inhibitor;

(b) Probing the human DNA library with at least one probe capable of binding to the protease inhibitor gene or its protein product;

(c) Identification of at least one clone containing the gene coding for the inhibitor by virtue of the ability of the clone to bind at least one probe for the gene or its protein product;

(d) Isolation of the gene coding for the inhibitor from the clone or clones identified; and

(e) Linking the gene, or suitable fragments thereof, to operational elements necessary to maintain and express the gene in a host microorganism.

13. The method of claim 12 wherein said cells are human parotid cells.

SUBSTITUTE SHEET

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14. The method of claim 3 wherein said natural DNA sequence is obtained by the method comprising:

- (a) Preparation of a human genomic DNA library;
- (b) Probing the human genomic DNA library with at least one probe capable of binding to a serine protein inhibitor gene or its protein product;
- (c) Identification of at least one clone containing the gene coding for the inhibitor by virtue of the ability of the clone to bind at least one probe for the gene or its protein product;
- (d) Isolation of the gene coding for the inhibitor from the clone or clones identified; and
- (e) Linking the gene, or suitable fragments thereof, to operational elements necessary to maintain and express the gene in a host microorganism.

15. A synthetic DNA sequence capable of directing microbial synthesis of a single polypeptide chain serine protease inhibitor having at least one active site possessing serine protease inhibitor activity, said protein exhibiting substantial homology to the native serine protease inhibitor isolated from parotid secretions.

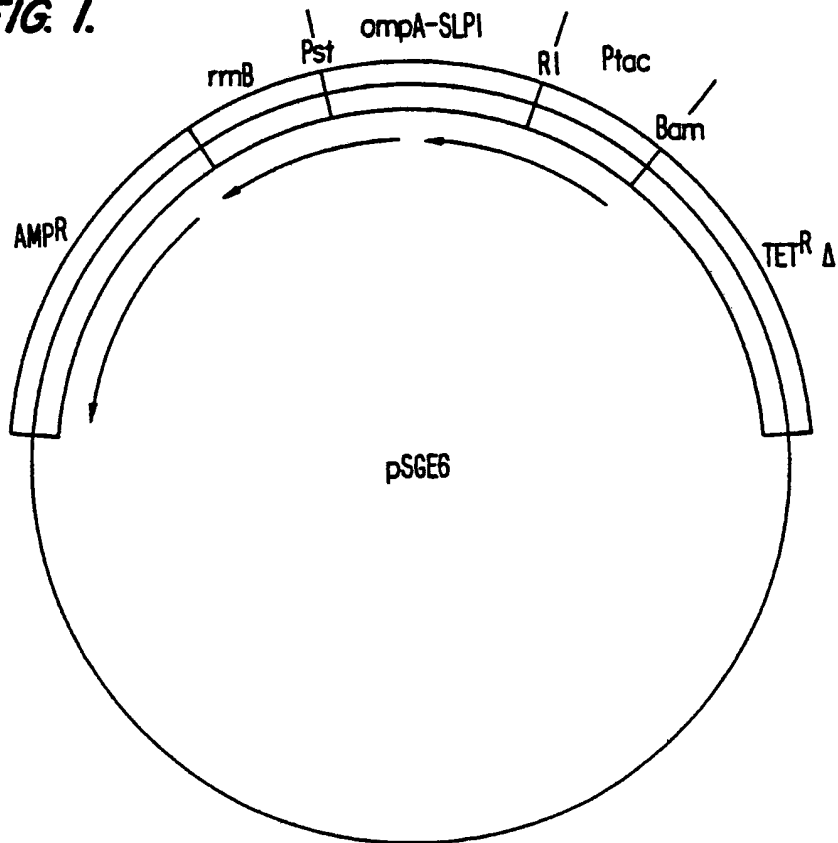
16. The DNA sequence of claim 15 wherein said sequence is selected from the group consisting of (1)

5'	AGCGG	TAAAA	GCTTC	AAAGC	TGGCG	TATGC	CCGCC
	GAAAA	AATCC	GCGCA	GTGTC	TGCGG	TACAA	AAAAC
	CGGAA	TGCCA	GTCCG	ACTGG	CAGTG	CCCGG	GTAAA
	AAACG	TTGTT	GCCCG	GACAC	CTGCG	GCATC	AAATG
	CCTGG	ATCCG	GTTGA	TACCC	CGAAC	CCGAC	TCGTC
	GAAAA	CCGGG	TAAAT	GCCCG	GTAAC	CTATG	GCCAG
	TGTCT	GATGC	TGAAC	CCGCC	GAAC	TCTGC	GAAAT
	GGACG	GCCAG	TGTAA	ACGAG	ATCTG	AAATG	CTGTA
	TGGGT	ATGTG	CGGCA	AATCT	TGTGT	TTCCC	CGGTA
	AAAGC	ATAA					3';

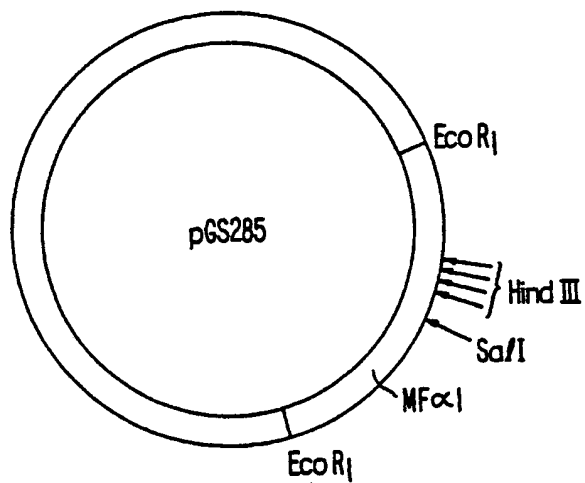
or (2) genetically equivalent sequences coding for production of the same protein.

17. A translational coupler having the nucleotide sequence TAACGAGGCGCAAAAAATGAAAAAGACAGCTATCGCGATCAAGGAGAAATAAATG.

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FIG. 1.**FIG. 3.**

DERIVED FROM pGS185
 < THE *EcoR*_I FRAGMENT
 CONTAINING THE α -FACTOR
 GENE FROM pCY17



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FIG. 2.

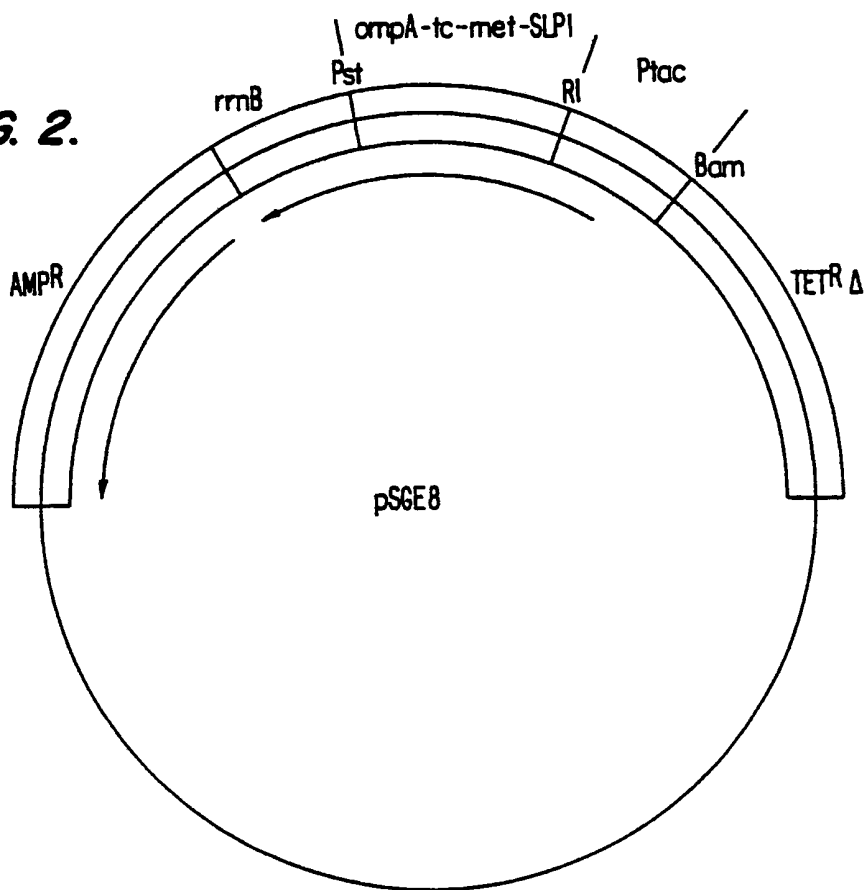
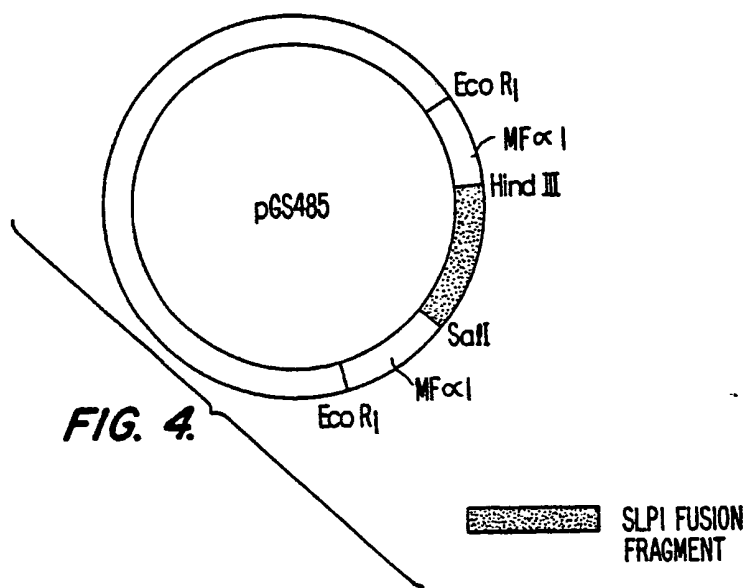
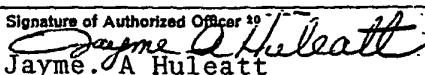
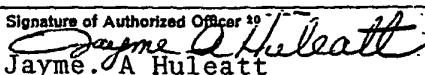
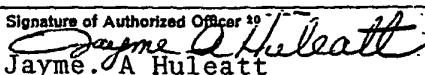


FIG. 4.



INTERNATIONAL SEARCH REPORT

International Application No PCT/US85/02385

I. CLASSIFICATION OF SUBJECT MATTER (If several classification symbols apply, indicate all) ³ According to International Patent Classification (IPC) or to both National Classification and IPC IPC4 C12P 21/00 435/68																				
II. FIELDS SEARCHED <div style="text-align: center; border-top: 1px solid black; border-bottom: 1px solid black;">Minimum Documentation Searched ⁴</div> <table style="width: 100%; border-collapse: collapse;"> <tr> <th style="width: 20%; border-bottom: 1px solid black;">Classification System</th> <th style="border-bottom: 1px solid black;">Classification Symbols</th> </tr> <tr> <td style="vertical-align: top; padding: 5px;">U.S.</td> <td style="padding: 5px;">435/68, 172.3, 253, 255, 317 536/27 935/6, 8, 9, 10, 18, 27, 37, 44, 45, 56, 69, 74, 75</td> </tr> </table> <div style="text-align: center; border-top: 1px solid black; border-bottom: 1px solid black;">Documentation Searched other than Minimum Documentation to the extent that such Documents are included in the Fields Searched ⁵</div>			Classification System	Classification Symbols	U.S.	435/68, 172.3, 253, 255, 317 536/27 935/6, 8, 9, 10, 18, 27, 37, 44, 45, 56, 69, 74, 75														
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CHEMICAL ABSTRACT DATA BASE (CAS) 1973-1986; BIOSIS DATA BASE 1969-1986; ORBIT-1982-1986; PROTEIN IDENTIFICATION RESOURCE DATA BASE																				
III. DOCUMENTS CONSIDERED TO BE RELEVANT ¹⁴ <table style="width: 100%; border-collapse: collapse;"> <tr> <th style="width: 10%; border-bottom: 1px solid black;">Category ⁶</th> <th style="border-bottom: 1px solid black;">Citation of Document, ¹⁵ with indication, where appropriate, of the relevant passages ¹⁷</th> <th style="width: 15%; border-bottom: 1px solid black;">Relevant to Claim No. ¹⁸</th> </tr> <tr> <td style="text-align: center; vertical-align: top; padding: 5px;">Y</td> <td style="padding: 5px;">N, Ohlsson, K. et al, <u>Chemical Abstracts</u>, Vol 99: 173443u, 1983.</td> <td style="text-align: center; vertical-align: top; padding: 5px;">1-16</td> </tr> <tr> <td style="text-align: center; vertical-align: top; padding: 5px;">Y</td> <td style="padding: 5px;">N, Schiessler, H. et al, <u>Chemical Abstracts</u>, Vol 90: 117084e, 1979</td> <td style="text-align: center; vertical-align: top; padding: 5px;">1-16</td> </tr> <tr> <td style="text-align: center; vertical-align: top; padding: 5px;">Y</td> <td style="padding: 5px;">N, Fritz, H. et al, <u>Chemical Abstracts</u>, Vol 88: 132417t, 1978</td> <td style="text-align: center; vertical-align: top; padding: 5px;">1-16</td> </tr> <tr> <td style="text-align: center; vertical-align: top; padding: 5px;">Y</td> <td style="padding: 5px;">N, Schiessler, H. et al, <u>Chemical Abstracts</u>, Vol 89: 192866u, 1978</td> <td style="text-align: center; vertical-align: top; padding: 5px;">1-16</td> </tr> <tr> <td style="text-align: center; vertical-align: top; padding: 5px;">Y</td> <td style="padding: 5px;">N, Rogers, J. et al, <u>Biochem. Biophys Res. Comm.</u>, Vol 116, pp 375-382, 1983</td> <td style="text-align: center; vertical-align: top; padding: 5px;">1-16</td> </tr> </table>			Category ⁶	Citation of Document, ¹⁵ with indication, where appropriate, of the relevant passages ¹⁷	Relevant to Claim No. ¹⁸	Y	N, Ohlsson, K. et al, <u>Chemical Abstracts</u> , Vol 99: 173443u, 1983.	1-16	Y	N, Schiessler, H. et al, <u>Chemical Abstracts</u> , Vol 90: 117084e, 1979	1-16	Y	N, Fritz, H. et al, <u>Chemical Abstracts</u> , Vol 88: 132417t, 1978	1-16	Y	N, Schiessler, H. et al, <u>Chemical Abstracts</u> , Vol 89: 192866u, 1978	1-16	Y	N, Rogers, J. et al, <u>Biochem. Biophys Res. Comm.</u> , Vol 116, pp 375-382, 1983	1-16
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<div style="display: flex; justify-content: space-between;"> <div style="width: 45%;"> <p>⁶ Special categories of cited documents: ¹⁶</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </div> <div style="width: 45%;"> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"A" document member of the same patent family</p> </div> </div>																				
IV. CERTIFICATION <table style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 50%; border-bottom: 1px solid black; padding: 5px;"> Date of the Actual Completion of the International Search ¹ <div style="text-align: center; padding: 5px;">14 February 1986</div> </td> <td style="width: 50%; border-bottom: 1px solid black; padding: 5px;"> Date of Mailing of this International Search Report ² <div style="text-align: center; padding: 5px;">21 FEB 1986</div> </td> </tr> <tr> <td style="border-bottom: 1px solid black; padding: 5px;"> International Searching Authority ¹ <div style="text-align: center; padding: 5px;">RO/US</div> </td> <td style="border-bottom: 1px solid black; padding: 5px;"> Signature of Authorized Officer ¹⁹ <div style="text-align: center; padding: 5px;">  Jayme A. Huleatt </div> </td> </tr> </table>			Date of the Actual Completion of the International Search ¹ <div style="text-align: center; padding: 5px;">14 February 1986</div>	Date of Mailing of this International Search Report ² <div style="text-align: center; padding: 5px;">21 FEB 1986</div>	International Searching Authority ¹ <div style="text-align: center; padding: 5px;">RO/US</div>	Signature of Authorized Officer ¹⁹ <div style="text-align: center; padding: 5px;">  Jayme A. Huleatt </div>														
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III. D CUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
Category *	Citation of Document, ¹⁶ with indication, where appropriate, of the relevant passages ¹⁷	Relevant to Claim No ¹⁸
Y	N, Shocat, D. et al, <u>J. Biological Chem</u> , Vol 253, pp 5630-5634, 1978	1-16
Y	Y EP, 103,409, Published 21 March 1984,	1-16
Y	Y Kurachi, K. et al, <u>Proc. Natl. Acad. Sci</u> , Vol 78, pp 6826-6830, 1981	1-16
A	N, Schoner, B, et al, <u>Proc. Natl. Acad. Sci.</u> , Vol 81, pp 5403-5407, 1984	17
A	DE, 3,247,922, Published 28 June 1984	17
A	N, Travis, J. et al, <u>Ann. Rev. Biochem</u> , Vol 52, pp 655-709, 1983	1-16